Tulip User Manual

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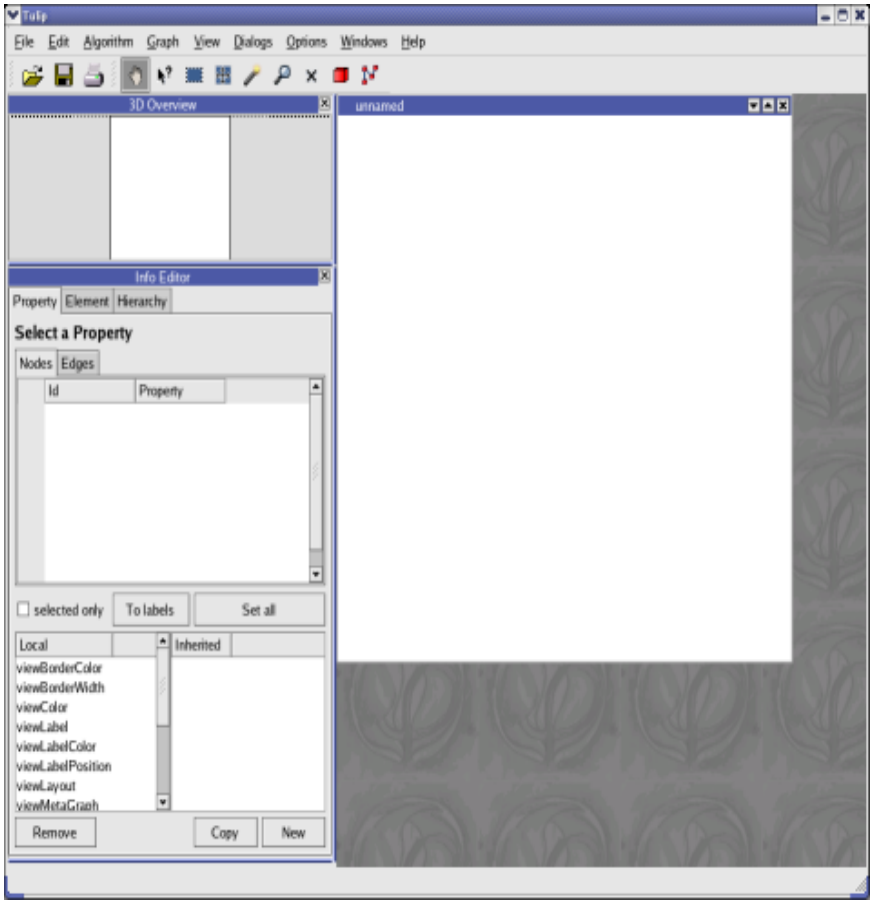
Chapter 1. Introduction

The research by the information visualization community show clearly that using a visual representation of datasets enables faster analysis by the end users. Tulip, created by David AUBER, is a contribution of the area of information visualization, “InfoViz”. Even if the Tulip framework enables the visualization, the drawing and the edition of small graphs, all the parts of the framework have been built in order to be able to visualize graphs having to 1.000.000 elements. A visualization system must draw and display huge graphs, enables to navigate through geometric operations as well as extracts subgraphs of the data and allows to change the representation of the results obtained by filtering.



Chapter 2. Graphic Interface

2.1. Main window : Menus

The main window of Tulip software is composed of several subwindows and a menu bar :

- `File`: this menu is used for usual file operations : New(**Ctrl+N**), Open(**Ctrl+O**), Save(**Ctrl+S**), Save As(**Ctrl+Shift+S**), Print(**Ctrl+P**) and Exit(**Ctrl+Q**). Others are added:
  - `Import`: this submenu is populated by import plugins.
    - `File` : Plugins allowing importation of graph files in different format such as Adjacent Matrix, gml, dot (graphviz), or tlp (tulip default file format).
    - `Graph` : Plugins allowing the creation of randomly generated graphs of different types.
    - `Misc` : Plugins to capture the tree structure of a file system directory, or the graph structure of a web site.
  - `Export`: this submenu is populated by export plugins allowing to save a tulip graph accordingly to a specified format. By default Tulip is able to export in GML and TLP formats.
  - `Save as picture`: this last menu gives the choice between different picture formats (BMP, EPS, JPEG, PBM, PGM, PNG, PPM, SVG, XBM, XPM) in wich graphs can be exported to.
- `Edit`: this is composed of tools : Cut(**Ctrl+X**), Copy(**Ctrl+C**), Paste(**Ctrl+V**) and Find(**Ctrl+F**), which affect the selected elements. This menu contains also: Select All(**Ctrl+A**), Delete selection(**Del**), Deselect all(**Ctrl+Shift+A**), Invert Selection(**Ctrl+I**), Create group(**Ctrl+G**), Create subgraph(**Ctrl+Shift+G**).More details on the `Find` tool : The find tool has 4 options :
  - Replace : Replace the current selection (nodes or edges already selected).
  - Add : Add the nodes (or edges) to be selected to the current selection.
  - Remove : Remove nodes (or edges) from the current selection.
  - Intersect : Select the intersection between the nodes (or edges) TO BE selected, and the ones from the current selection.
- `Algorithm`: this one is divided in several parts to make a difference between the kind of algorithms you can apply. These are:
  - `Selection`: this submenu is populated by 'selection' algorithms. These algorithms allows to select nodes and or edges (assign the 'viewSelection' property see Section 3.3, "Properties of graph" for more details) satifying some criteria. For example the 'Loop Selection' algorithm detects all edges for which the starting and ending nodes are the same.
  - `Color`: this submenu is populated by 'color' algorithms. These king of algorithm computes the color (the 'viewColor' property see Section 3.3, "Properties of graph" for more details) of the graph elements. A default one, 'Metric Mapping', is provided; it allows to color all graph elements according to a metric property.

- `Measure`: this submenu is populated by 'metric' algorithms. These algorithms allows to compute and assigned a value to the 'viewMetric' property of graph elements see Section 3.3, "Properties of graph" for more details. For example, when running the 'Degree' algorithm, the degree (the number of its neighbors) is compute and assigned to each graph node 'viewMetric' property.

- `Layout`: this submenu is populated by 'layout' algorithms which allow to display graphs using different types of drawings. For example, the 'Circular' algorithm places all nodes of a graph along a circle. Before :

After :

- `Size`: this submenu is populated by 'size' algorithms which allow to compute the size (the 'viewSize' property see Section 3.3, "Properties of graph" for more details) of the graph elements.

- `General`: this submenu is populated by more general algorithms for computing properties, subgraphs, quotient graphs, groups... For example the 'Equal Value' algorithm create subgraphs for which the included elements have the same value for a choosed 'metric' property.

For more information please visit Section 3.2, "Algorithms"

- `Graph` : This menu is composed of 2 sub menus :

  - `Tests`: This sub menu contains tools able to say if the graph obey some constraints :

    - `Simple` : Is the Graph Simple ? For more information please visit : Wikipedia: Simple graphs[1]

    - `Directed Tree` : A directed tree is a directed graph which would be a tree if the directions on the edges were ignored. Some authors restrict the phrase to the case where the edges are all directed towards a particular vertex, or all directed away from a particular vertex. For more information please visit : Wikipedia: Directed Tree[2]

    - `Free Tree`: A tree without any designated root is called a free tree. For more information please visit : Wikipedia: Simple graphs[3]

    - `Acyclic` : A graph is acyclic if it contains no cycle. A cycle is a path that as the same source and target. For more information please visit : Wikipedia: Acyclic graphs[4]

    - `Connected` : A graph is called connected if every pair of vertices in the graph is connected. For more information please visit : Wikipedia: Connectivity [5]

    - `Bi-connected` : A connected graph is biconnected if the removal of any single node and his out edges can not disconnect the graph. For more information please visit :Wikipedia: Biconnected Graphs [6]

    - `Tri-connected` : If it is always possible to establish a path from any node to an other one even after removing any 2 nodes, then the graph is said to be Tri-connected. For more information please visit : Wikipedia: k-connected graphs [7]

[1] http://en.wikipedia.org/wiki/Simple_graph#Simple_graph
[2] http://en.wikipedia.org/wiki/Directed_tree
[3] http://en.wikipedia.org/wiki/Free_tree
[4] http://en.wikipedia.org/wiki/Acyclic_Graph
[5] http://en.wikipedia.org/wiki/Connected_graph
[6] http://en.wikipedia.org/wiki/Biconnected_graph
[7] http://en.wikipedia.org/wiki/K-connected_graph

- `Planar` : A graph is said to be planar if it can be drawn on the (Euclidean) plane without any edges crossing. Wikipedia : Planar Graphs[8]

- `Modify` : Those operations will modify the entire structure of a graph .

  - `Make Simple` : This algorithm will change the graph to make it a simple graph. For more information please visit : Wikipedia: Simple graphs[9]

  - `Make Acyclic` : A graph is acyclic if it contains no cycle. A cycle is a path that as the same source and target. For more information please visit : Wikipedia: Acyclic graphs[10]

  - `Make Connected` : A graph is said to be connected if every pair of vertices in the graph is connected. For more information please visit : Wikipedia: Connectivity [11]

  - `Make Bi-connected` : For more information please visit : Wikipedia: Biconnected Graphs [12]

  - `Make directed` : If the graph is a free tree, make it directed. If a node and only one node is selected, this one will be considered as the root node. If none is selected, Tulip will heuristically choose the center of the graph as the root node. For more information please visit : Wikipedia: Directed Tree[13]

  - Reverse selected edges : Exchange source and target of an edge.

`View`: this is composed of the operations about a view. It is possible to redraw, center the current view, create a new 3D view (initially a copy of the current one) (Section 2.7, “New 3D View”)

- `Dialogs`: this menu allows to redisplay each of the dialog windows such as the info editor window, or the 3D overview.

- `Windows`: this menu contains two options for the management of the views in the workspace : cascade or tile mode.

- `Options`: this menu allows to enable/disable the display options:

  - Force ratio : Tries to keep a good Height/Width ratio for the layout of the graph.

  - Map metric : Applies the Color / Metric Mapping algorithm, whenever, a measure algorithm has been run.

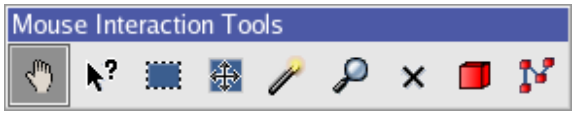
  - Morphing : Enables the Morphing from a layout to an other.

  - Tooltips : Enables the display of tooltips on nodes or edges

  - Grid : Shows the grid configuration dialog.

- `Help`: in this menu, you can find informations about the software and the way to make your first steps.

2.2. Mouse Interaction Toolbar



This toolbar allows to select the mouse operation you want to perform. Operations are listed and explained, from left to right of the toolbar :

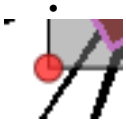
[8] http://en.wikipedia.org/wiki/Planar_graph
[9] http://en.wikipedia.org/wiki/Simple_graph#Simple_graph
[10] http://en.wikipedia.org/wiki/Acyclic_Graph
[11] http://en.wikipedia.org/wiki/Connected_graph
[12] http://en.wikipedia.org/wiki/Biconnected_graph
[13] http://en.wikipedia.org/wiki/Directed_tree

`3D Navigation` : This tool enables the 3D navigation on a graph using the mouse movements (left button pressed); the available operations are: translate, rotate, zoom, zoom and pan. Translation is the default operation and can also be activated using the Arrow keys; rotation is activated using **Shift** key, zoom is activated using **Ctrl** key (**Alt** key on Mac), zoom and pan is activated using the wheel of the mouse (**APPLE** key on Mac). Warning, the last operation is 'mouse position centered'; i.e it attempts to translate the last 2D or 3D position of the mouse to the center of the view.

`Get Information` : when this operation is selected, if you click on an element of a graph (node or edge), Tulip displays all available properties of that node/edge using the `Element` tab of the `Info Editor` sub-window (see Section 2.5, "Info Editor").

`Rectangle Selection` : Allows multiple elements selection. Elements within the selection box are selected. If **Shift** key is pressed, the newly selected elements are added to the current selection, if **Ctrl** key (**Alt** key on Mac) is pressed, the selected elements are removed from the current selection; else they replace the current selection.

`Selection edition` : This tool allows to modify the current selection. Available operations are horizontal stretch, vertical stretch, all axis stretch, coordinate axis rotation and translation. If no key is pressed, coordinates are modified. If **Shift** key is pressed, only coordinates are modified. If **Ctrl** is pressed, only size is modified.A left button click outside the selection box reset the selection.



Press on this 'circle' to rotate the selection.

Press on this 'triangle' to change width or height of the selection.

The 'square' is used both for resizing AND rotating the selection.

`Magic Selection` : it enables to select all the graph connected nodes having the same metric. It works like the magic selection in image editing software. The difference is the topology of the graph.

`Zoom Box` : It enables to zoom on a defined rectangle area. The first corner of the rectangle is defined when pressing the mouse left button, the opposite corner is defined when moving the mouse and the zoom operation is performed on the desired rectangle when the button is released.

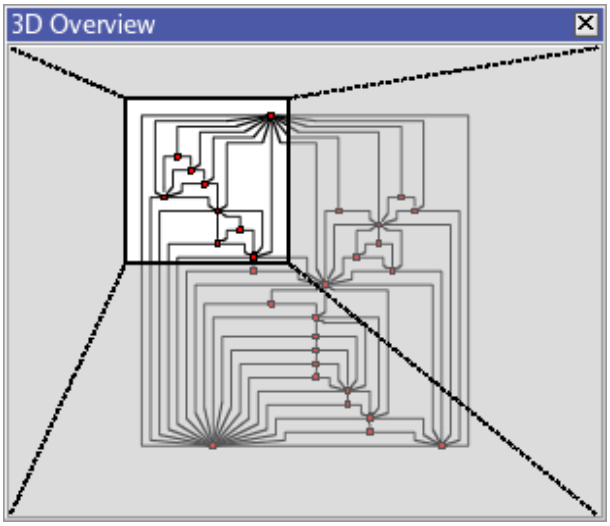
`Delete element` : allows to delete a node or edge by a simple click. The deleted node or edge is the one under the mouse when you clicked.

`Add node` : when it is selected, you can add a node in the graph by a simple mouse click on the current graph view. The node is placed at the coordinates corresponding to the mouse position when you clicked.

`Add edge` : when it is selected, you can add an edge in the graph by mouse clicking first on the source node then on the target node.

2.3. 3D Overview

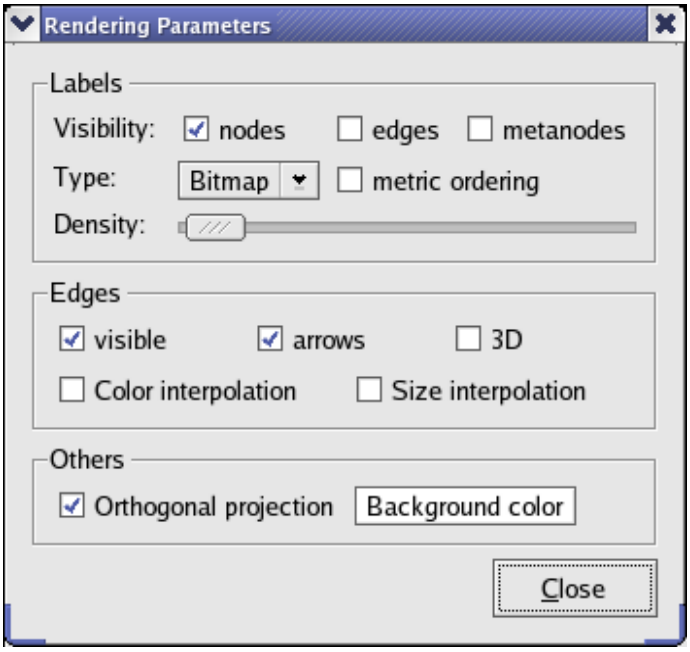
This subwindow always shows an overview of the current graph view.



The part of the graph which is visible in the current view is inside a black bordered frame. In order to see a different part of the graph in the current view, you can move the frame over the desired part. To achieve this, when the mouse is inside the frame, just move it with the left button pressed. A mouse left click with the **Ctrl** key pressed (**Alt** key on Mac) displays the Rendering Parameters dialog (see Section 2.4, “Rendering Parameters”).

2.4. Rendering Parameters

All actions in this dialog are just performed for the current view window.



This dialog is diaplayed when clicking on the `Dialogs->Rendering Parameters`(**Ctrl+R**). Ienables to configure the rendering of the graph. The available options are grouped in the following three frames:

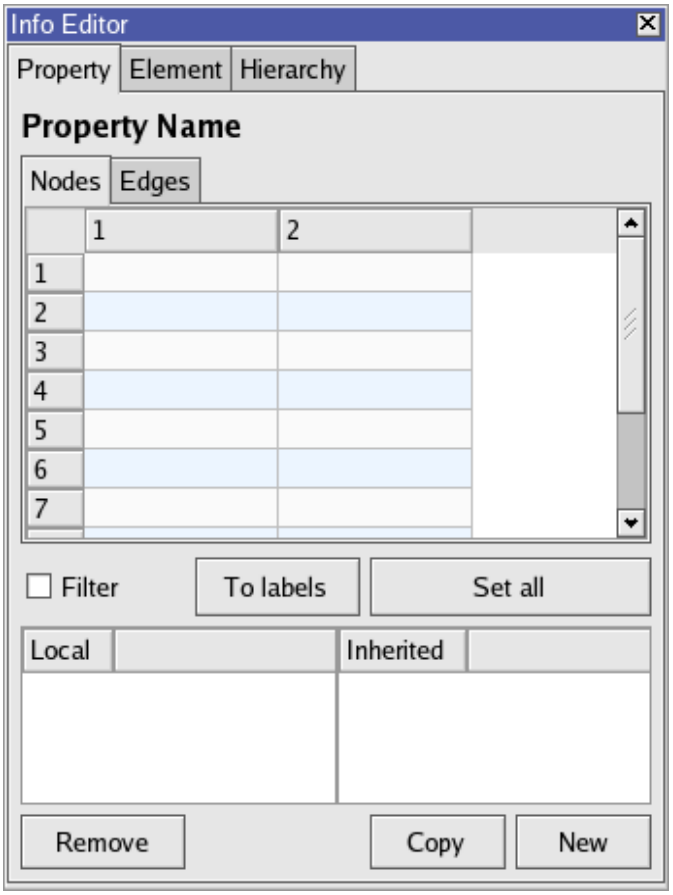
- `Labels` : the options in this frame only affect the display of the labels:
  - `Visibility` : you can enable/disable the display of labels on nodes, edges or metanodes.
  - `Type` : this indicates the text display mode which can be one of Bitmap, Texture or 3D.
  - `metric ordering` : when checked the labels are displayed in using the viewMetric property decreasing order.
  - `Density` : use this slider to avoid having too much labels displayed (max is on the left).
- `Edges` : this frame options affect the way the edges are displayed:
  - `visible` : enables/disables the display of edges. If not checked, the other options of this frame are not active.
  - `arrows` : enables/disables the display of arrows.
  - `3D` : enables/disables the display of edges in 3D.
  - `Color interpolation` : when checked the edge color is interpolated from the color of its source node to the color of its target node.
  - `Size interpolation` : when checked the edge size is interpolated from the size of its source node to the size of its target node.
- `Others` : the options in this frame are related to general aspects of the rendering:
  - `Orthogonal projection` : enables/disables the orthogonal projection. If not checked, the perpsective projection is used.
  - `Background color` : enables to choose a color for the background of a graph view.

2.5. Info Editor

This subwindow is divided in four tabs : Property, Element, Hierarchy, Statistics (not displayed in the standard version).

2.5.1. Property

This tab enables to display the properties of nodes and edges as a table. It is composed of two parts. The one of the top of the tab displays all the values of nodes or edges for the selected property (choosen in the lists at the bottom of the tab). It is possible to display only the values of the selected elements by using the `selected only` box. The user can modify directly a value by clicking on the value in the table. It is possible to set all the nodes or edges value with the `Set all` button; if the `selected only` box is checked, this will only affect the selected elements. An other possibility is to set as labels the values of the selected property by clicking on the `To labels` button. The bottom part of the tab displays the lists of all the local and inherited properties of a graph. An inherited property is a property which is defined for an upper graph in the hierarchy of graphs (see Section 2.5.3, “Hierarchy”).



By a right mouse button press (press **Ctrl** key when mouse pressing on Mac) on a row of the table values, you can display a pop-up menu allowing some actions on the graph element corresponding to the table row:

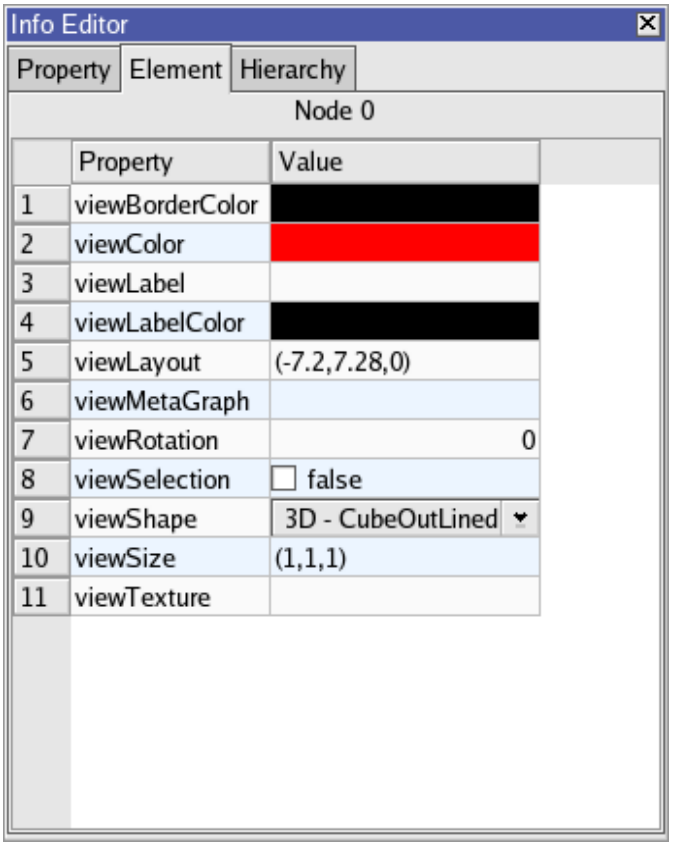
- `Add to/Remove from selection` : this allows to change the selection state of the element,
- `Select` : the current element replaces the whole selection,
- `Delete` : this permanently removes the element from the current graph,
- `Properties` : this shows the element properties in the “Element” tab (see after).

For more details please visit : Section 3.3, “Properties of graph”

2.5.2. Element

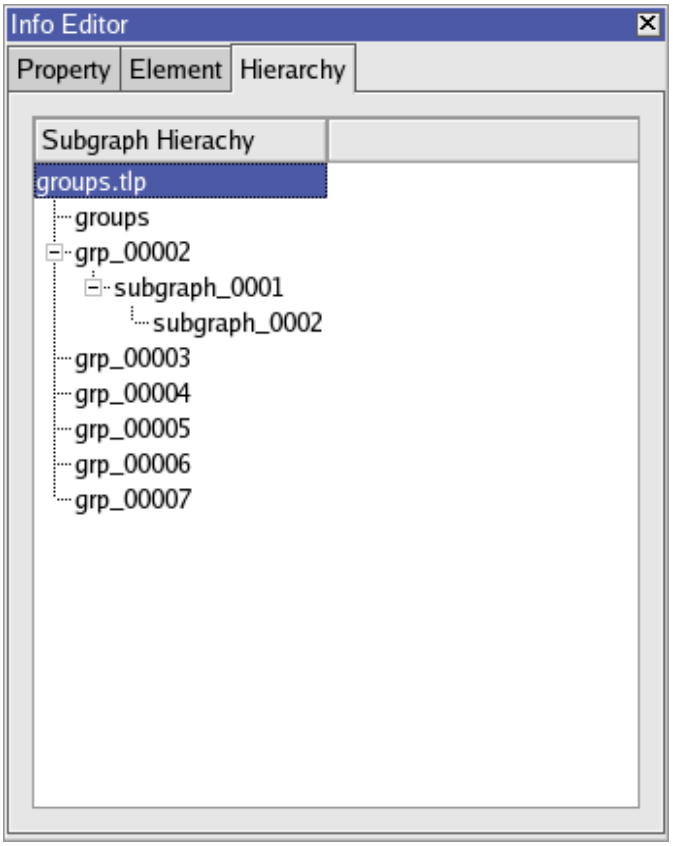
This tab shows informations about an element of the graph, node or edge, previously "pointed" using the

mouse toolbar operation. At the top, you can find the type of the element and its “id”. To follow, here is the table displaying the elements properties and associated values. As within the tables of the “Property” tab, it is possible to update the values within this table.



2.5.3. Hierarchy

This tab shows the inclusion relationships betweeen the different existing subgraphs and groups of a graph. All of them could be created with the Tulip tools. A hierarchy of graph is often the result of the computation of clustering algorithms.



By a right mouse button press (press **Ctrl** key when mouse pressing on Mac) in the hierarchy display, you can display a pop-up menu allowing to remove, clone, rename, a graph (subgraph or group).

2.5.4. Statistics (not available in standard version)

The statistics panel is composed of three main parts : Computation, Display and Clustering. It allows the user to compute a histogram or a scatter plot from a graph and one up to three metrics. The display part of the panel is used to display on screen the statistics main values (as Average point, Standard deviation, Bounding box, Linear Regression and Eigenvectors). The clustering part is used to display a clustering plane from a statistical value (previously computed) and to separate the graph into two new clusters : what is above the clustering plane (sup) and what is under the clustering plane (inf)

Figure 2.1. Computation Tab

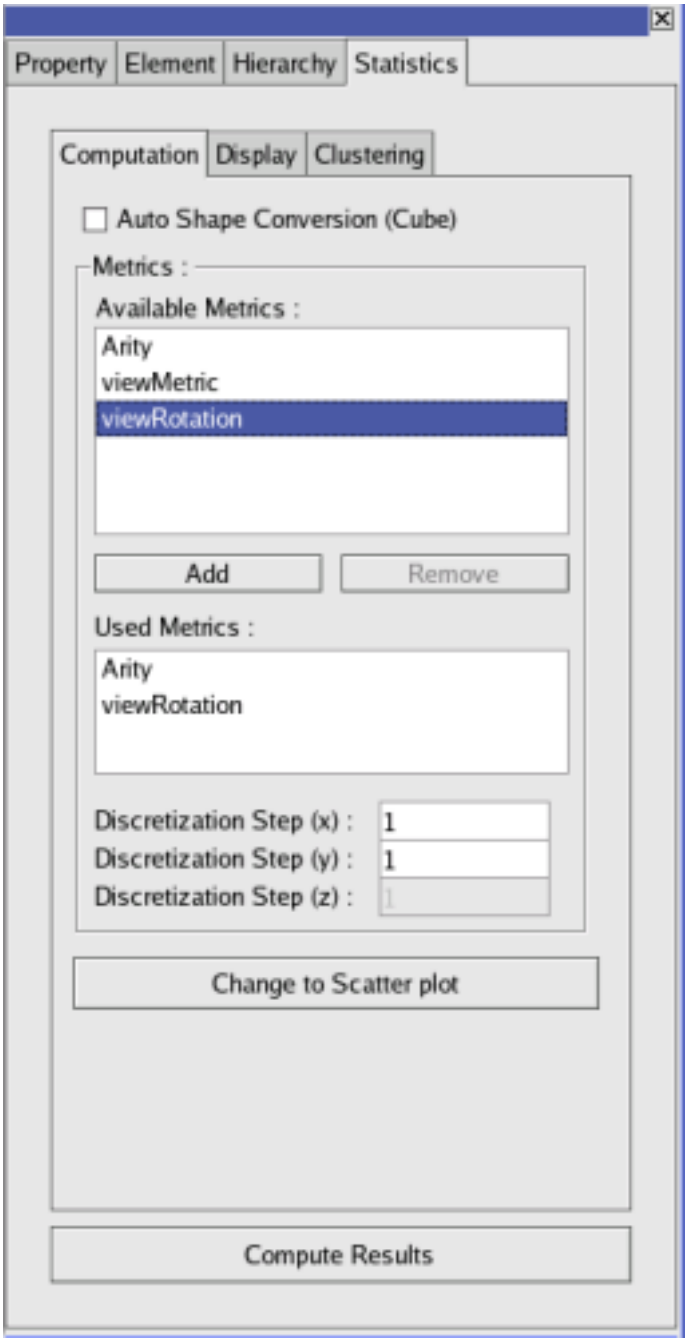


Figure 2.2. Display Tab

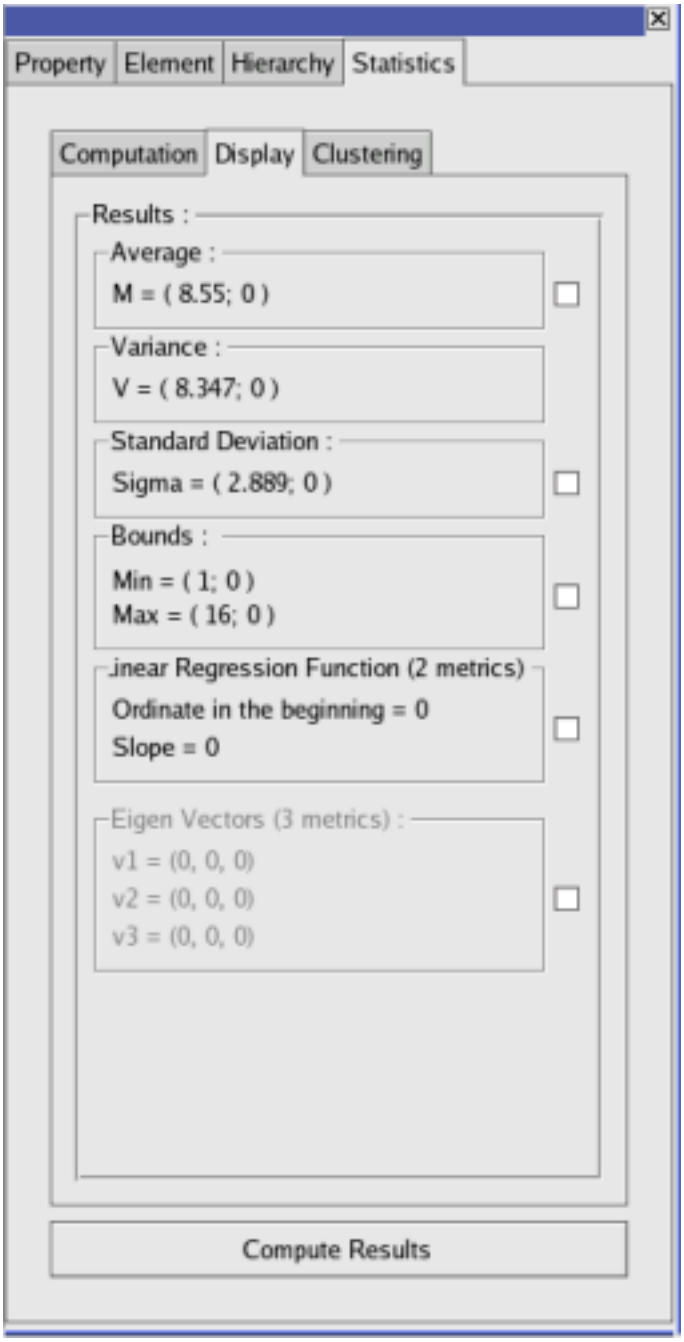
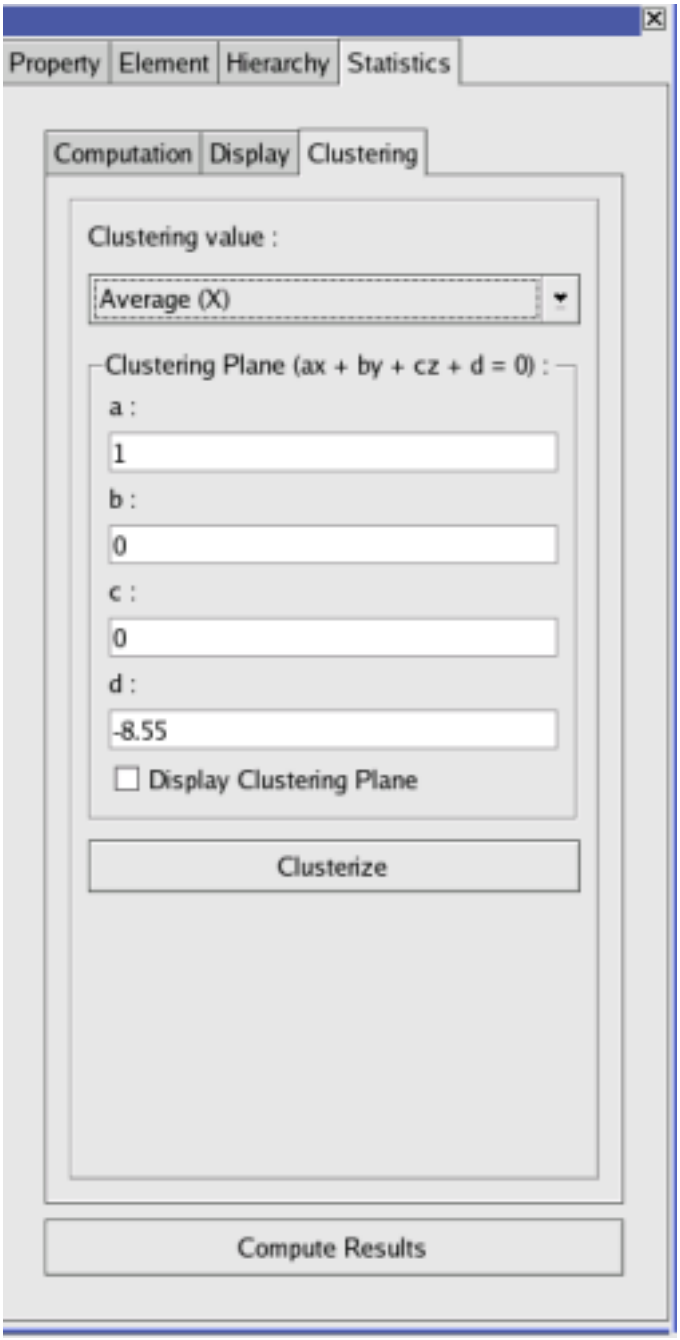
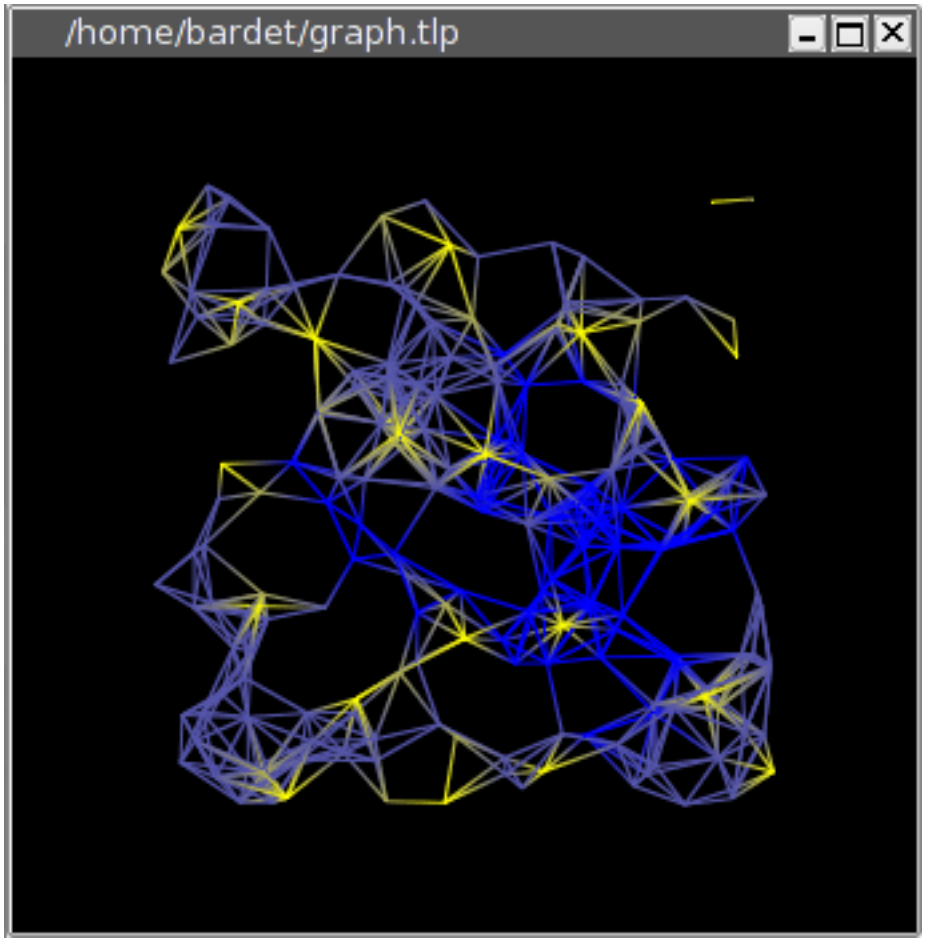


Figure 2.3. ClusteringTab



2.6. View window



The 3D graph view subwindow is the window where the graph is displayed. It can display graph in two or three dimensions and enables to apply the mouse operations selected in the tool bar by directly clicking on the drawing of the graph. If the user lets the mouse during few seconds on a node/edge, a tooltip window displays its id and label (use “Options” menu to enable tooltips).

2.6.1. Pop-up menu of graph view

This pop-up menu is displayed when pressing on the mouse right button (press **Ctrl** key when mouse pressing on Mac) while on a graph element, and allows to perform simple actions on this element :

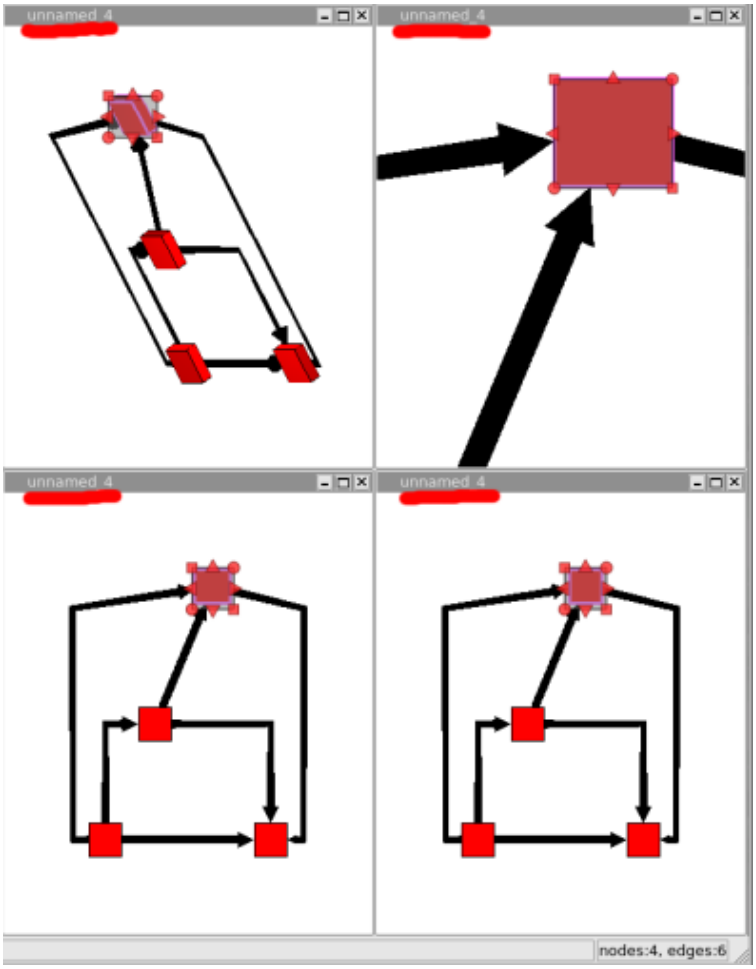
- `Add to/Remove from selection` : this allows to change the selection state of the element,

- `Select` : the current element replaces the whole selection,
- `Delete` : this permanently removes the element from the current graph,
- `Go inside` : if the element is a metanode, this shows the corresponding subgraph in the current view,
- `Ungroup` : if the element is a metanode, this permanently removes it and its corresponding subgraph,
- `Properties` : this shows the element properties in the “Element” tab.

2.7. New 3D View

A very useful tool in Tulip is the `View->New 3D View`. This tool will create a new window with the same name, and the same graph as before. But this window, is not a copy of the original one. It is just another view of the graph.

For example, if you zoom in forward a node on the second window. nothing will change on the other one. But if you delete a node on the second window, it will be deleted in the original window.



Chapter 3. Functionalities

3.1. Management of Graphs

Tulip software offers a way to create and manage graphs. The main window enables to have several 3D views to show differents graphs. The menu bar enables the user to create a new view. In there and with the mouse toolbar, the users can create nodes and edges at the place where the pointer is. When you have a graph and you want to keep traces of the graph, you can save it in the `.tlp` format, of Tulip Software. An other option is to export it in the `GML` format, for the graphlet system, a toolkit for graph editors and graph algorithms. Then, you can save as an picture the result you had. Tulip supports different formats : BMP, EPS, JPEG, PBM, PGM, PNG, PPM, SVG, XBM, XPM.

Tulip could generate a graph from data : importation.

Examples of importation

- Adjacency Matrix : a form of representation of graphs. Please visit Wikipedia: Adjacency Matrix[1] for more details.
- File System : make a graph with your file system ; the root is the directory you have selected.
- GML import : create a graph from this other format.
- dot : create a graph from *graphviz* format.

The second possibility is to generate automatically different kinds of graph : Graph, Tree, Grid, which could be complete, simple, uniform, ...

Examples of generation

- Complete General Graph
- Complete Tree
- Grid
- Grid approximation
- Random General Graph
- Random Simple Graph
- Uniform Random Binary Tree

[1] http://en.wikipedia.org/wiki/Adjacency_matrix

It is posssible to do a “Copy-Paste”. You can cut, copy and paste selected elements from a view. When you paste an element, it is placed at the same location it was in the original view. Use `View->Center View` (**Ctrl+Shift+C**) to make it visible in the second view. The menus and the mouse toolbar allow you to select the operation you want to perform on the selection.

3.1.1. The “Find” tool

In the `Edit` menu, it exists a `Find` item allowing to do some requests on the current graph. The tool gives a way to choose the desired property and the action you want perform regarding the current selection: Make out of the found elements a new selection, Add them to the selection, Remove them from the selection or Intersect them with the current selection.

3.2. Algorithms

Each graph can be modified with algorithms for the layout, the set of selected elements, the size of nodes, the value attributed to an element (node or edge) named metric, the colors. An other advantage of Tulip is that it is easy to add a new algorithm in the structure; this way, it is able to include lot of algorithms. As explain in the Section 2.1, “Main window : Menus”, the algorithms are accessed by the `Algorithms` menu. Several categories are in there : Selection, Color, Layout, Measure, Size, General. They modify the properties of the graph elements.

3.2.1. Selection Algorithms

3.2.1.1. Induced Sub-Graph :

The induced Sub-Graph algorithm can be used to obtain the edges that are between selected nodes.
Here is an example :

`Before :`

`After :`

Algorithm documentation[2]

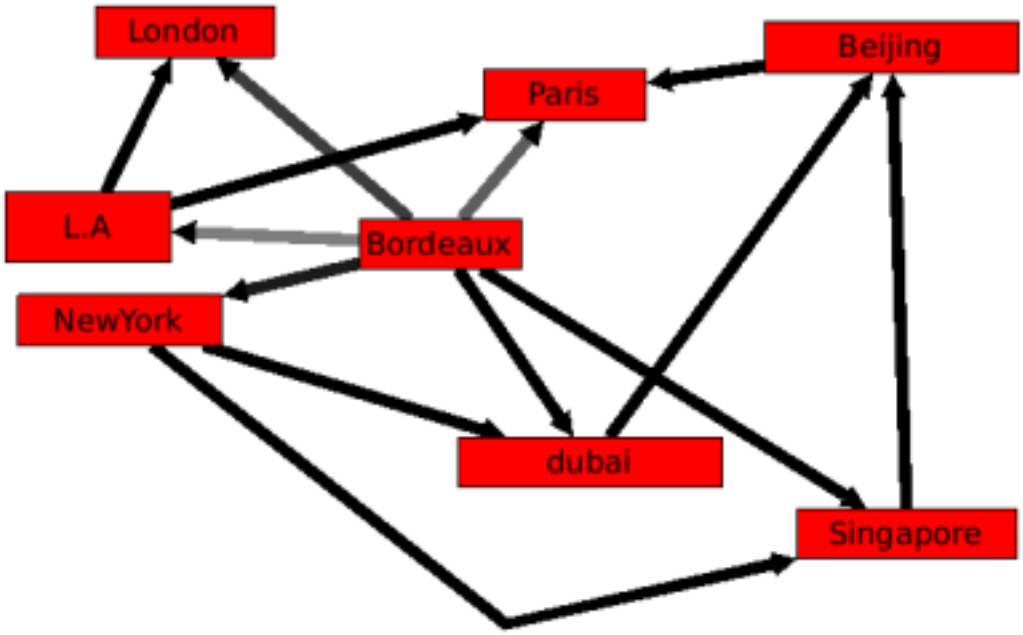
3.2.1.2. Kruskal :

The Algorithm of Kruskal is used to create a minimum spanning tree out of a connected graph.

It is divided in several steps :

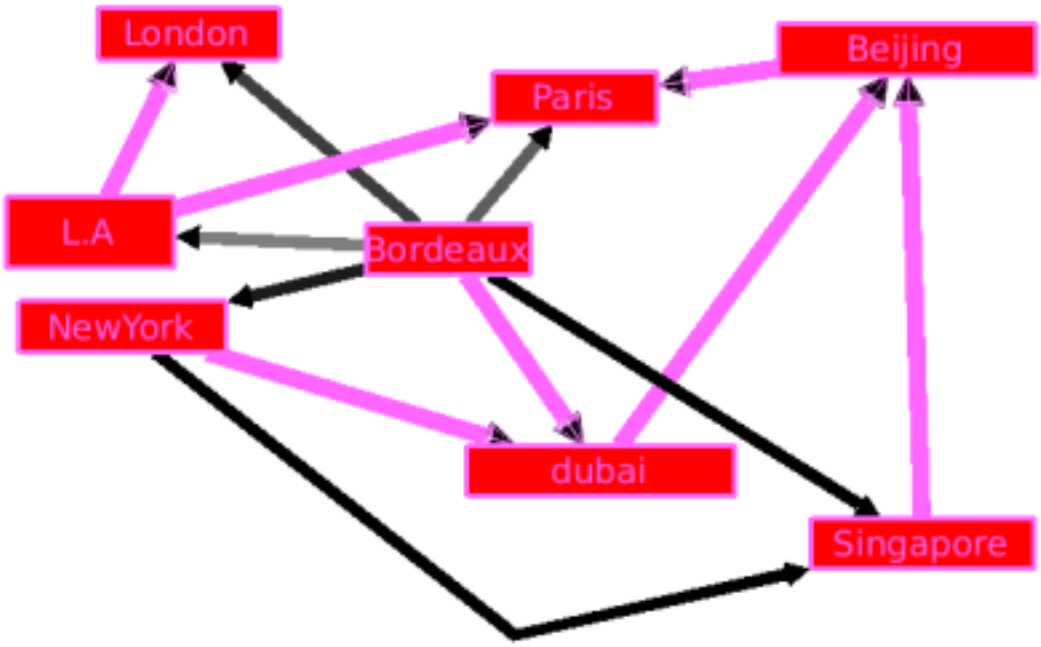
- Make a list of the edges starting with the "shortest" one, ending with the "longest one".
- Add all edges with their from/to nodes to the tree as long as you don't have any cycle.

Let's take an example : We have a set of airports, Bordeaux, Paris, L.A ..., the nodes, and a set of Airports connections, the edges.

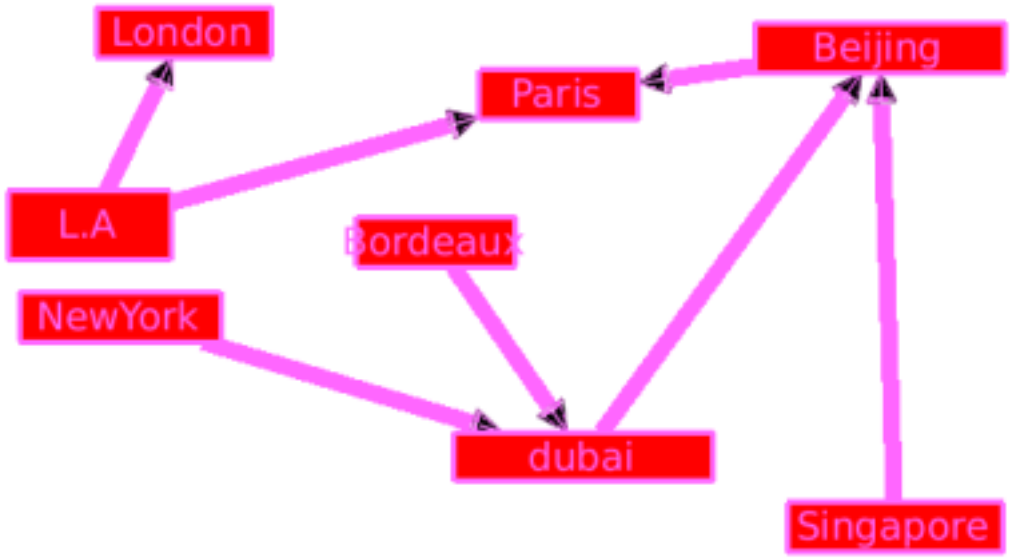


As you can see, this makes a very complicated Graph. As edges do not all have the same weight (in terms of price, distance, ...), some of them are not really important (the ones with a high weight). The algorithm of kruskal will select the ones that we can't remove.

[2] ../../doxygen/allPlugins.html#InducedSubGraphSelection



By creating a sub-graph we get a simple graph which is much more easy to read.



Please visit Wikipedia : Kruskal's algorithm [3] for more details.

Algorithm documentation[4]

3.2.1.3. Loop Selection :

This selection algorithm is able to select the loops of a graph. A loop is an edge that has the same source and target.

[3] http://en.wikipedia.org/wiki/Kruskal%27s_algorithm
[4] ../../doxygen/allPlugins.html#Kruskal

Algorithm documentation[5]

3.2.1.4. Multiple Edge :

This selection algorithm highlights the multiple-edges also named parallel-edges in a graph.

Two edges are parallel only if they both have the same target and same source.
Algorithm documentation[6]

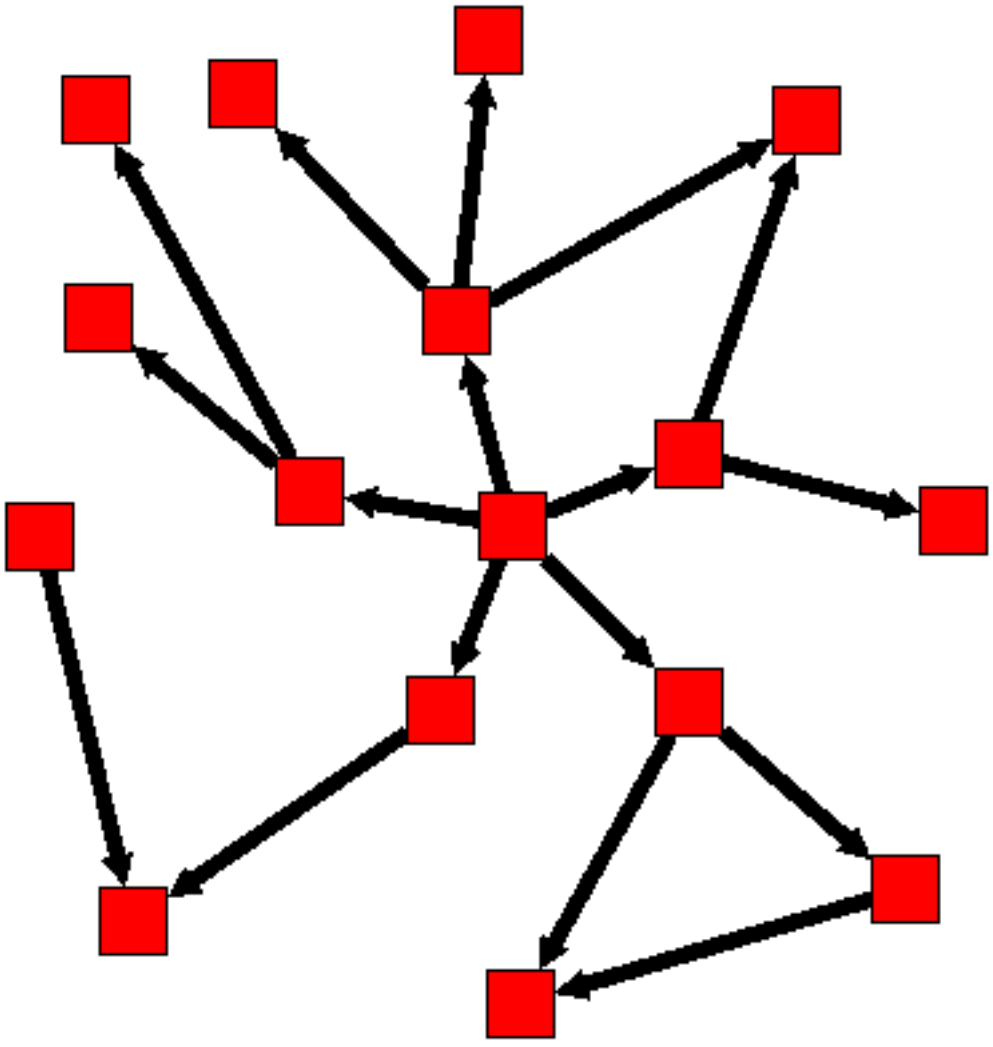
3.2.1.5. Reachable Sub-Graph :

This selection algorithm enables to find all nodes and edges at a fixed distance of a set of nodes. It takes three parameters :

- `Distance` : number of edges to follow.
- `Direction` : 0 means directed, 1 reverse directed, 2 undirected
- `Starting nodes` : the selected nodes of this selection property (boolean) will be used as starting nodes.

In the following example, 'distance' equals to 1, 'direction' equals 0, and the starting node is the one in the center.

`Before :`



[5] ../../doxygen/allPlugins.html#LoopSelection
[6] ../../doxygen/allPlugins.html#MultipleEdgeSelection

Func-
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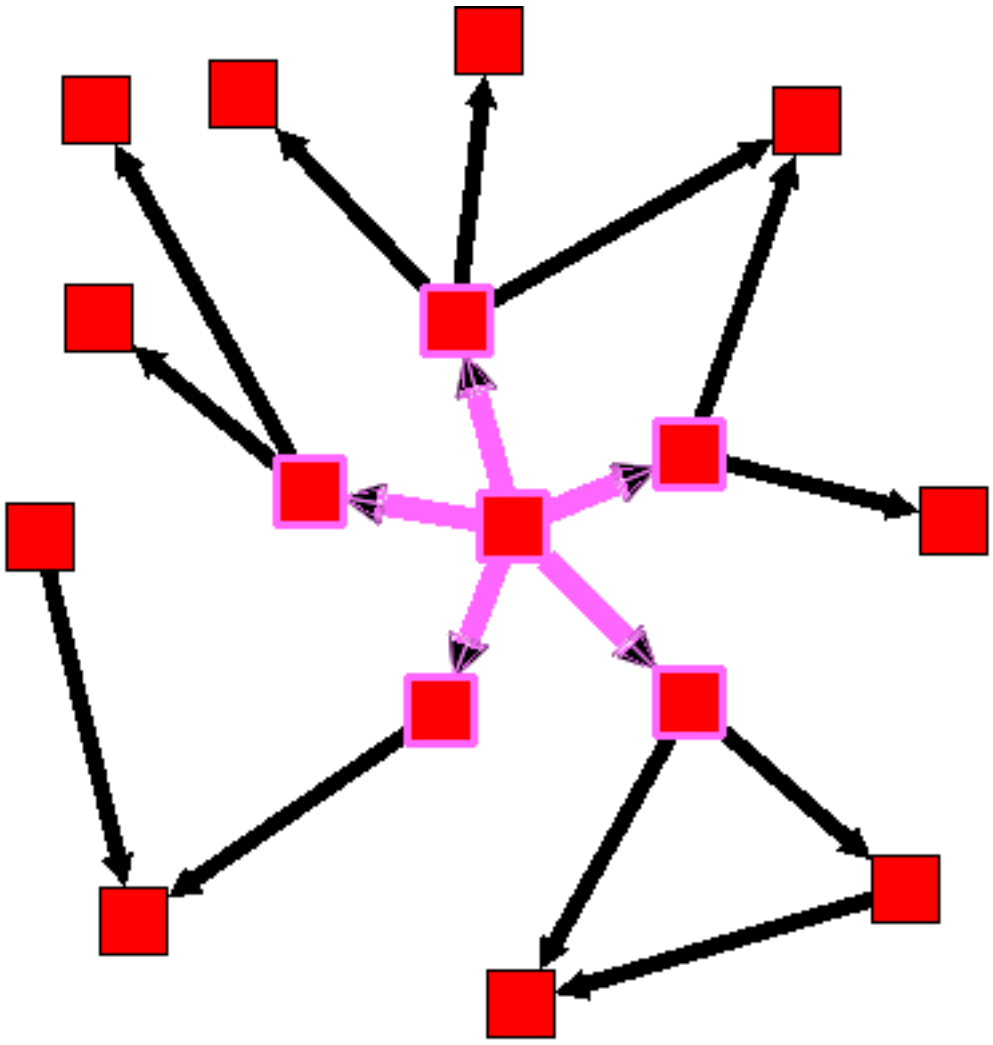
After :



Algorithm documentation[7]

3.2.1.6. Spanning Dag :

This selection algorithm can be used to select a sub-graph without any cycle.
Algorithm documentation[8]

3.2.1.7. Spanning Forest :

This algorithm can be used to create a set of spanning trees out of the graph.
A tree is a special kind of graph that has the following properties :

- Has a root (a starting point node).
- A node have severals sons and their is only one edges targeting each sons.
- Doesn't have any cycle.
- A leaf is an "ending node".

[7] ../../doxygen/allPlugins.html#ReachableSubGraphSelection
[8] ../../doxygen/allPlugins.html#SpanningDagSelection

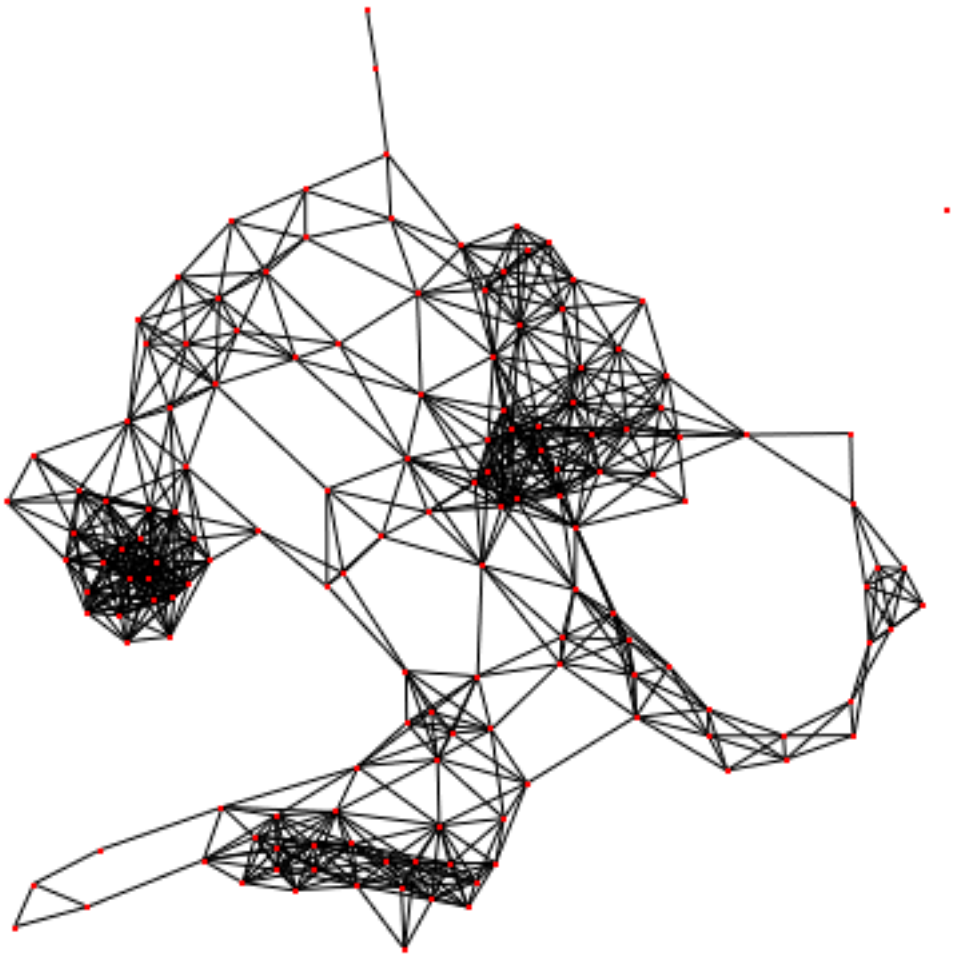
3.2.2. Color Algorithms :

3.2.2.1. Metric Mapping :

The metric mapping algorithm can be used to re-color the nodes of the graph after using a measure (Section 3.2.3, “Measure”) algorithm.
This Algorithm takes 5 parameters :

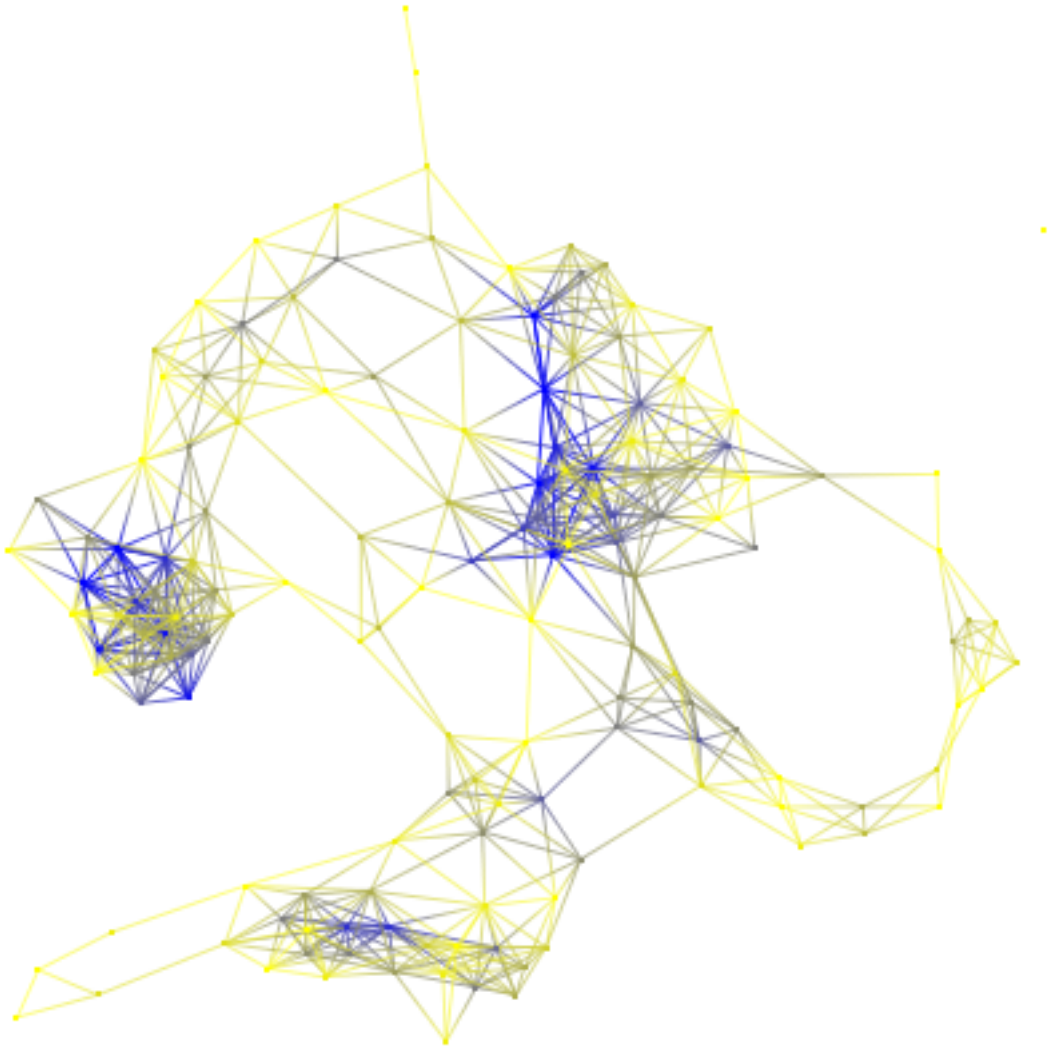
- `Property` : Property is a metric value. It is used to affect scalar values to graph items.
- `Colormodel` : Color can be either 1 or 0. 1 for RGB interpolation and 0 for HSV interpolation.
- `Type` : If type is checked, the color mapping will be uniform, which means that if you have 2 nodes with the property value equals to 0, there will be 2 nodes colored in "color1" . If type is not checked, the color quantification will be linear, which means that if you have 2 nodes with the property value equals to 0, there will be 1 node colored in "color1" and an other with a lighter color1.
- `Color1` : Color1 will be the color of the node that has the lowest value (according to the Property field)
- `Color2` : Color2 will be the color of the node that has the highest value (according to the Property field)

Let’s take an example :
As you can see here is a graph where no metric values has been computed.

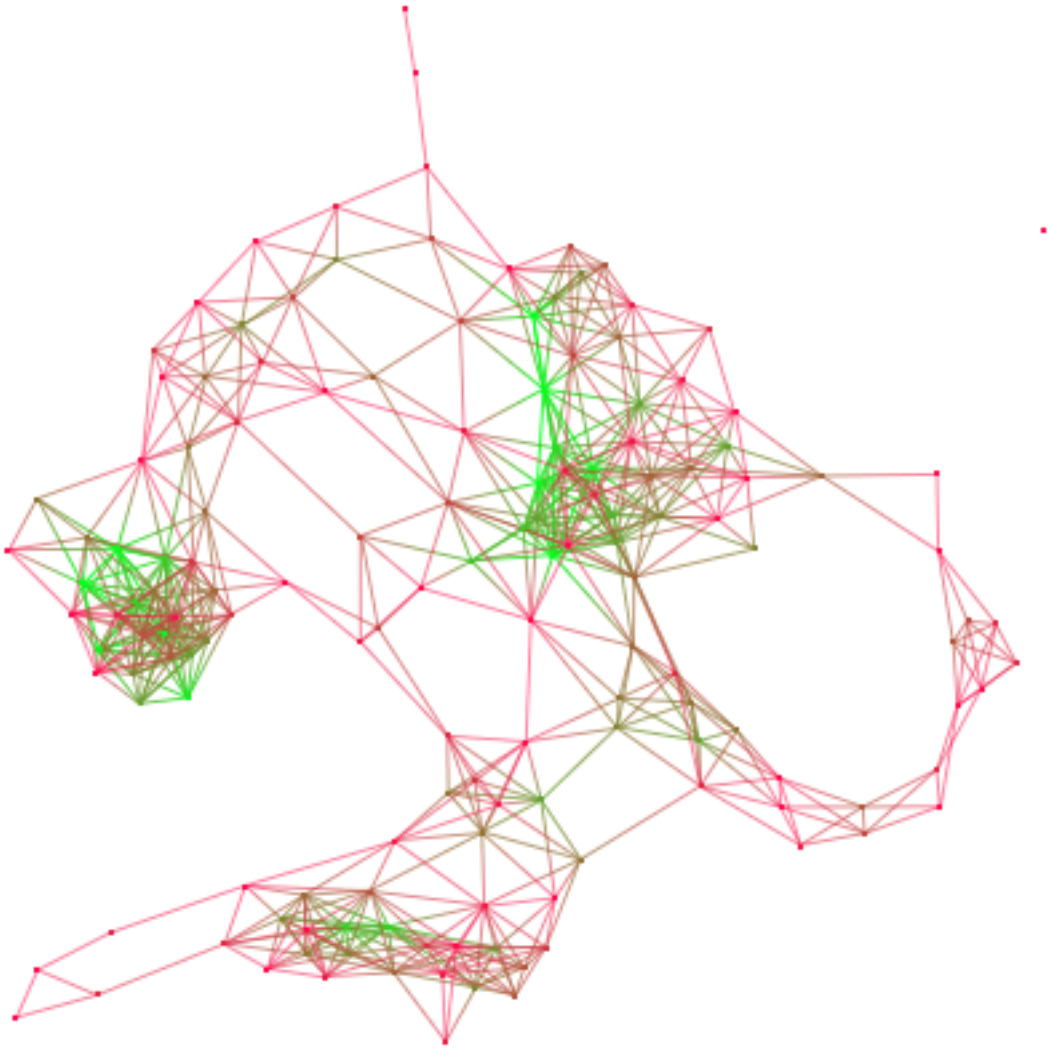


[9] ../../doxygen/allPlugins.html#SpanningTreeSelection

After applying the degree algorithm, the graph gets colors !



If you do not have any colors (on edges), see if you have checked the "Color interpolation" in the rendering parameters window (**CTRL+R**) . After applying the "Metric mapping" algorithm ("type" checked, "colormodel" equaled to 1 , "Color1", a kind of red and "Color2" a kind of green) we will obtain the following graph.



3.2.3. Measure

Measure algorithms are used to compute different metrics (on edges or nodes). The computed values are assigned to the viewMetric property.

3.2.3.1. Graph :

3.2.3.1.1. Betweenness Centrality :

Betweenness is a centrality measure of a node within a graph. Nodes that occur on many shortest paths between other nodes, have higher betweenness metric than those that do not. As this algorithm will compute a global measure, it can take a long time to finish. See Widipedia : Betweenness[10] for more details.

Algorithm documentation[11]

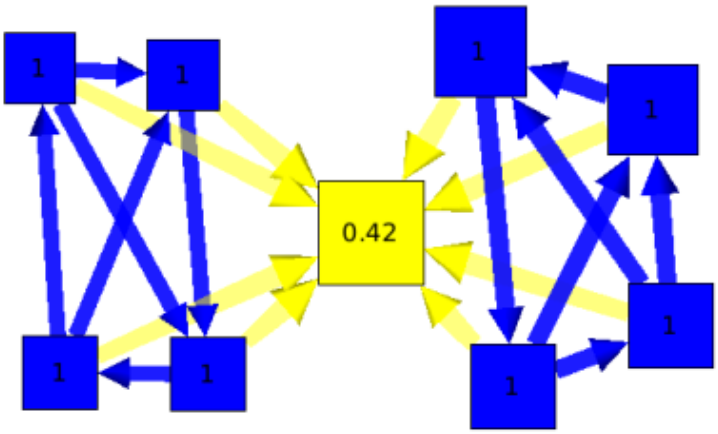
3.2.3.1.2. Cluster :

This algorithm can only be used on simple graphs (graphs with no loops).

The cluster algorithm is a measure algorithm that can determine whether or not a graph is a "small-world network". The clustering measure is a local measure that gives the connections rate of a node and its neighbors.

Let's take an example :

[10] http://en.wikipedia.org/wiki/Betweenness
[11] ../../doxygen/allPlugins.html#BetweennessCentrality



On this graph, and by looking at the clustering measure, you can see 2 "communities" (nodes in blue) and a hub (node in yellow).the hub is the only way to connect the two communities.

For more details, please visit http://en.wikipedia.org/wiki/Clustering_coefficient.
Algorithm documentation[12]

3.2.3.1.3. Degree :

This algorithm will save the degree of each node in its viewMetric property. It takes two parameters :

- Type : Is the type of degree you want to compute. In : Edges that comes onto the node. Out : Edges that are going away from the node. InOut : Using both (in and out).
- Metric : This parameter can take all double properties, but by default it will take : None, 'viewBorderWidth', 'viewMetric' and 'viewRotation'. If you choose none, the degree of the node will be the sum of the edges. If you choose the 'viewMetric' value, degree of the node will be the sum of edges wiewMetric property. As of viewBorderWidth and viewRotation.

3.2.3.1.4. Eccentricity :

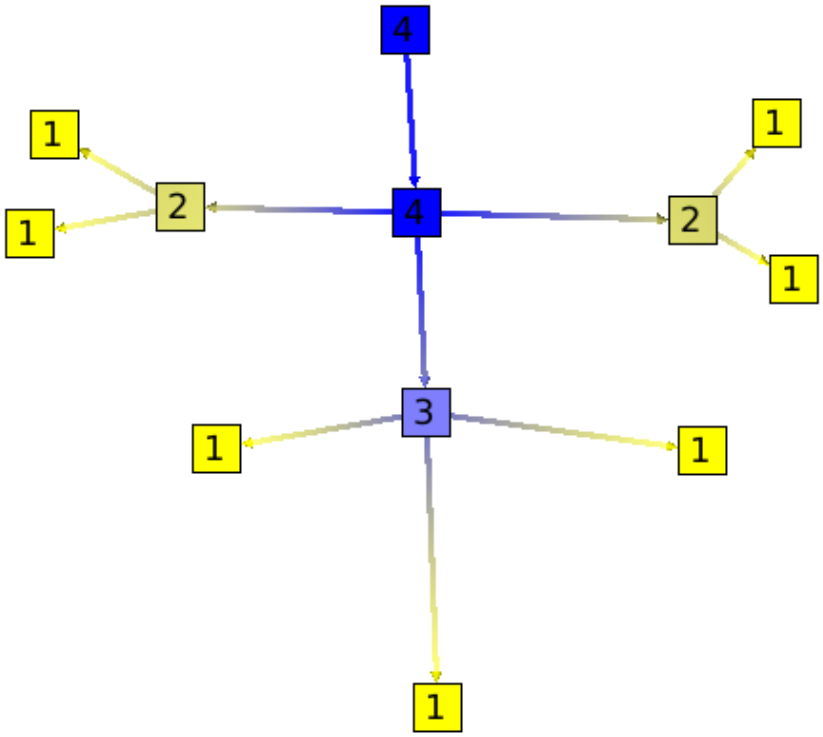
This plug in compute the eccentricity of each node, eccentricity is the maximum distance to go from a node to all others. In this version the value is normalized (1 means that a node is in the center of the network, 0 means that a node is the more eccentric in the network). The eccentricity will be saved in the viewMetric property of each node.
Algorithm documentation[13]

3.2.3.1.5. Strahler :

The Strahler algorithm is very powerful. It can for example point out important path in a graph, by computing for each node the degree of ramification of its (spanning) sub-tree. Following is a graph with only one path. You can see that each node have the same Strahler number (1).

[12] ../../doxygen/allPlugins.html#ClusterMetric
[13] ../../doxygen/allPlugins.html#EccentricityMetric

But on this graph, more the degree of ramification is important and more the number of strahler will be high.



Note that this graph could represent anything, a program (inclusion of sources files), or a city road traffic.

Functionalities

Parameters :

- All nodes : If not checked, the algorithm will choose a node (a source node) and will apply the algorithm to this node only. If checked, the algorithm will be applied to all nodes.
- Type :This parameter can take 3 different values : Register which will force the algorithm to give an indication on the degree of ramification (for trees), Stack, that will force the algorithm to give an indication on the number of nested cycles (for graphs), and at last, All, that will ask the algorithm to use both registers and stack.

For more information please visit http://en.wikipedia.org/wiki/Strahler_Stream_Order
Algorithm documentation[14]

3.2.3.1.6. Strength :

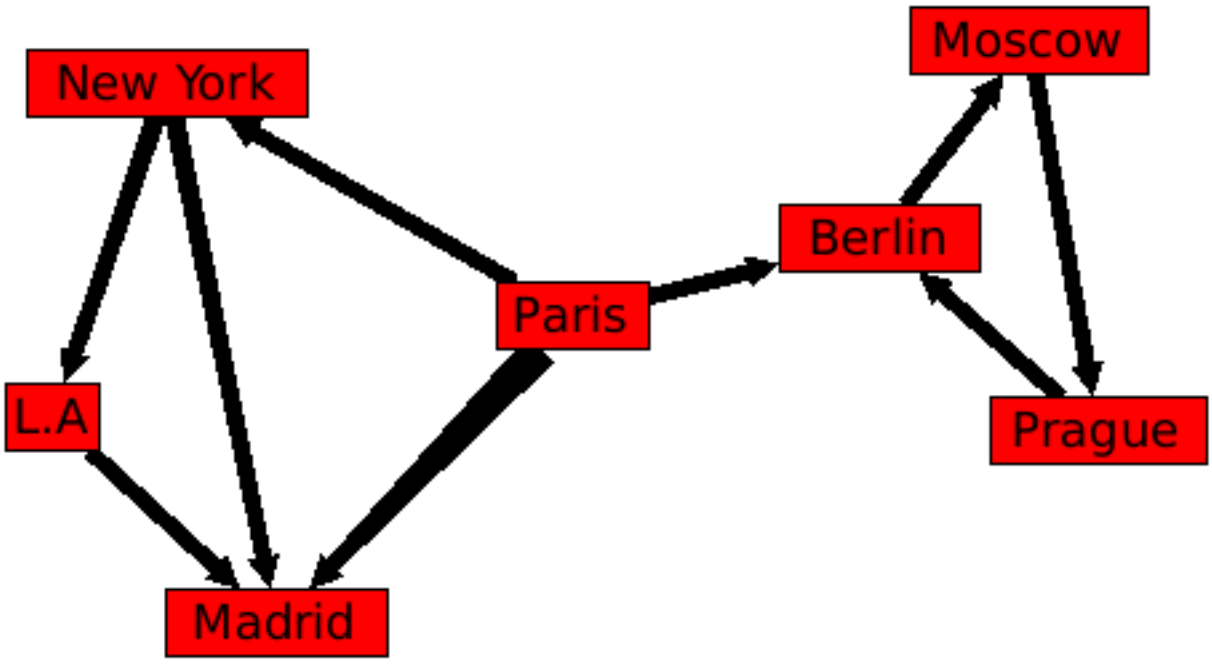
Graph must be simple (no loops).

This algorithm will compute the strength of edges. Every edges with small values are important in the way that their removal can disconnect two connected components. Every edges with a high value metric may belong to a strongly connected component.
Algorithm documentation[15]

3.2.3.2. Component :

3.2.3.2.1. Biconnected Component :

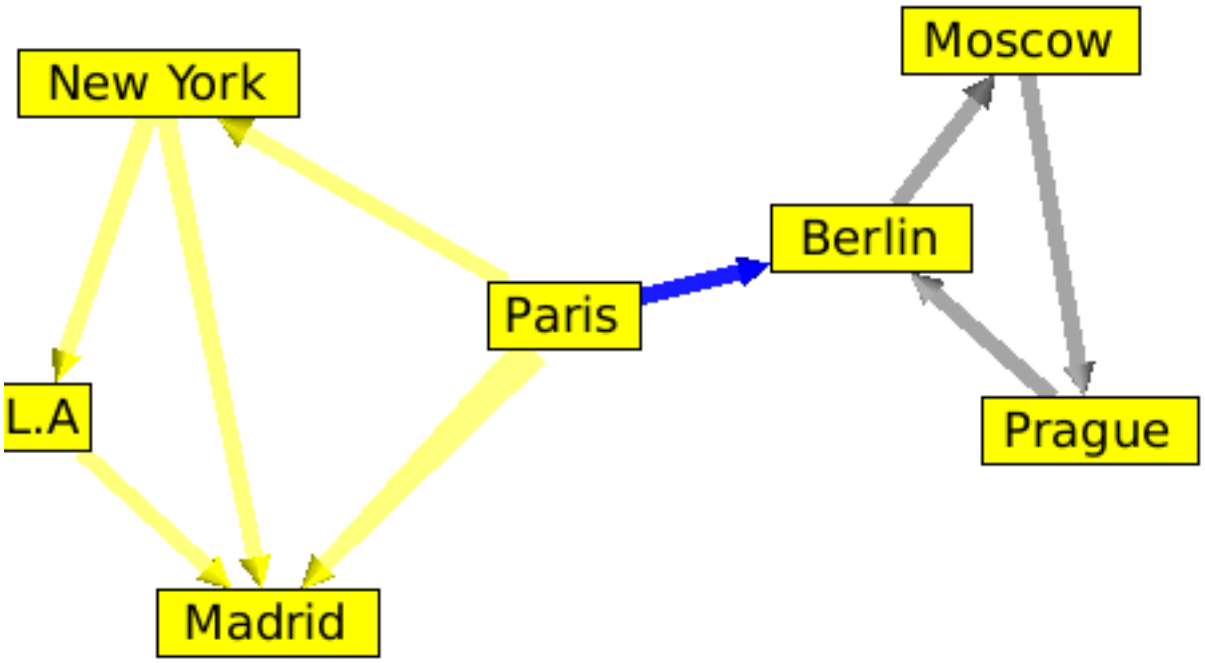
A connected graph is biconnected if the removal of any single node and his edges can not disconnect the graph. The biconnected components of a graph are the maximal subsets of nodes such that the removal of a node from a particular component will not disconnect the component. Note that unlike connected components, a node can belong to multiple biconnected components. For example we can use this algorithm on an airlines graph. Such as the one following.



[14] ../../doxygen/allPlugins.html#StrahlerMetric
[15] ../../doxygen/allPlugins.html#StrengthMetric

The result is, 3 biconnected components :

- : Paris, New York, L.A, Madrid.
- : Paris, Berlin.
- : Berlin, Moscow, Prague.



The intersection of those 3 biconnected components is Berlin and Paris. Which means that Berlin and Paris are two articulation points of our graph. Algorithm documentation[16]

3.2.3.2.2. Connected Component:

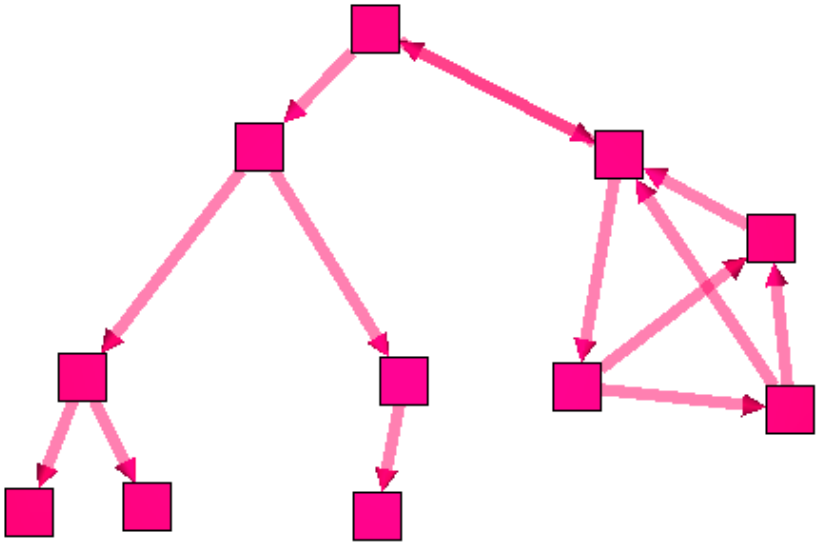
A connected component is a maximal connected subgraph. Two nodes are in the same connected component if and only if there exists a path between them.

After running the algorithm, the index of the connected component of a node is saved in its viewMetric property. It is the same for the edges.
For more details please visit : Wikipedia:Connected Component[17]Algorithm documentation[18]

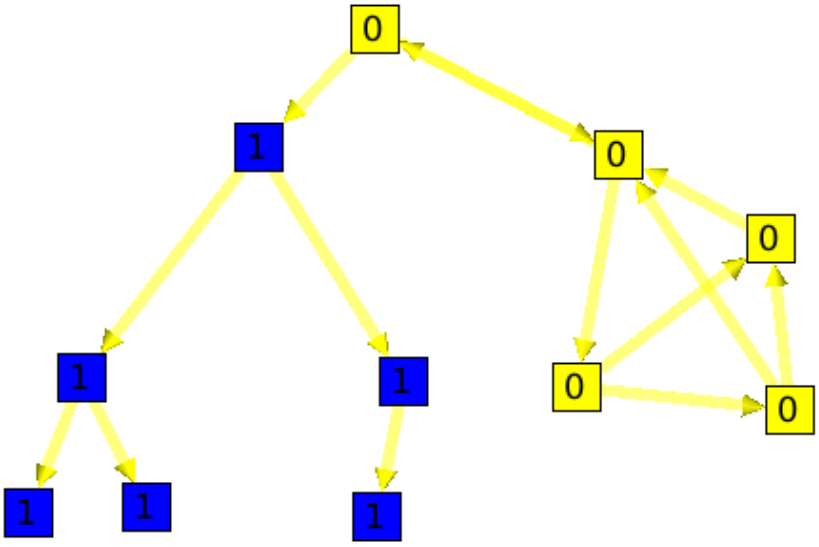
3.2.3.2.3. Connected Tree Component :

The connected tree component algorithm can be useful to find parts of a graph that are trees. Here is an example : Following is a graph with on the left side, a tree. This graph forms a unique connected component.

[16] ../../doxygen/allPlugins.html#BiconnectedComponnent
[17] http://en.wikipedia.org/wiki/Connected_component_(graph_theory)
[18] ../../doxygen/allPlugins.html#ConnectedComponent



As you can see, the algorithm divided the graph into 2 components.



Algorithm documentation[19]

3.2.3.2.4. Strongly Connected Component :

A directed graph is said to be strongly connected if for every pair of nodes S1 and S2, it exists two edges e1 and e2 such as :

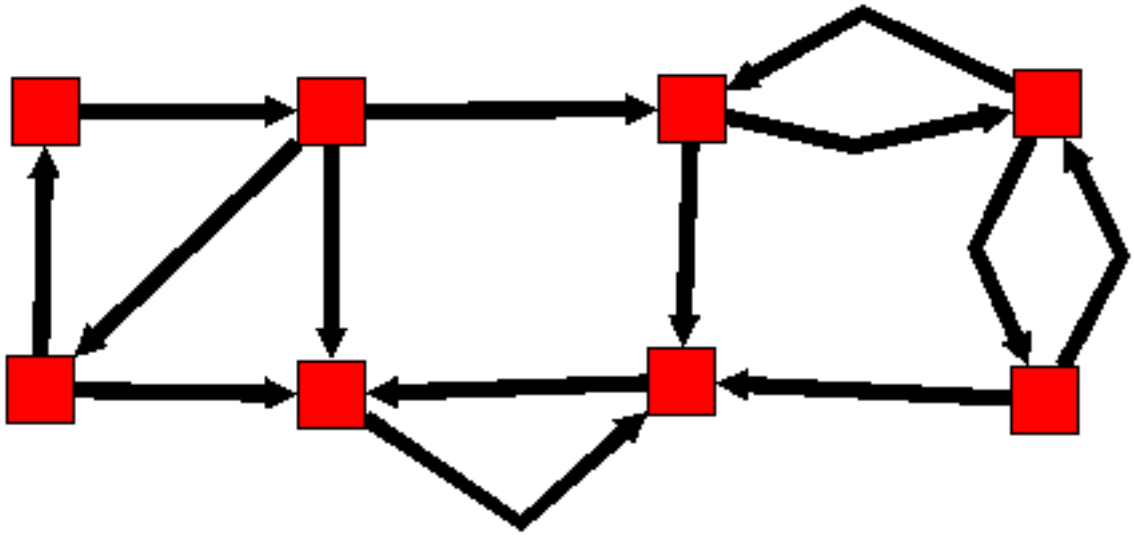
- The Source of e1 is S1 and Target is S2 .
- The Source of e2 is S2 and Target is S1.

[19] ../../doxygen/allPlugins.html#ConnectedAndTreeComponent

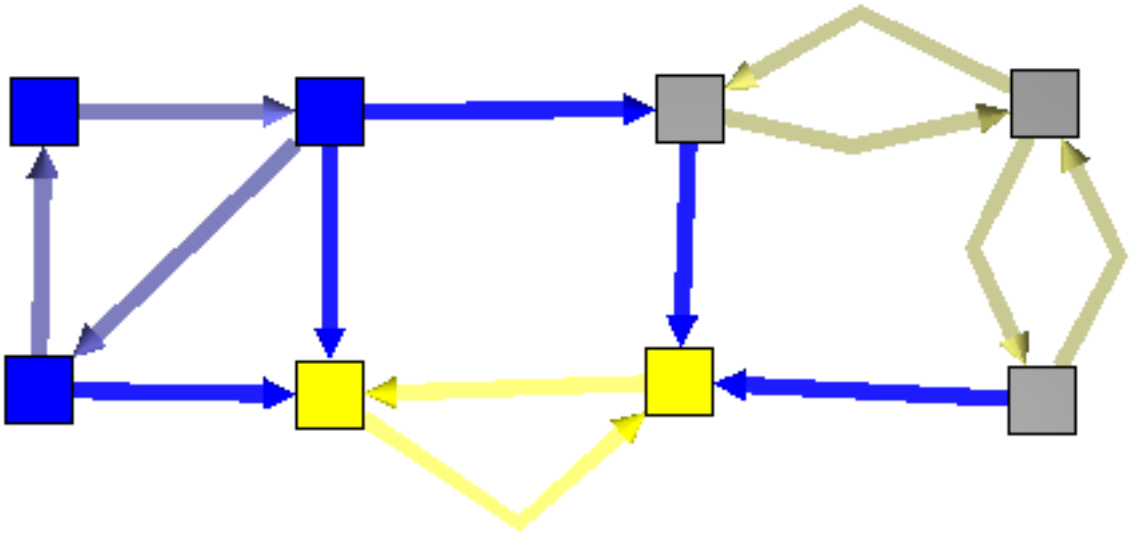
The strongly connected components of a directed graph are its maximal strongly connected subgraphs.

These form a partition of the graph.
Here is an example :

`Before :`



`After :`

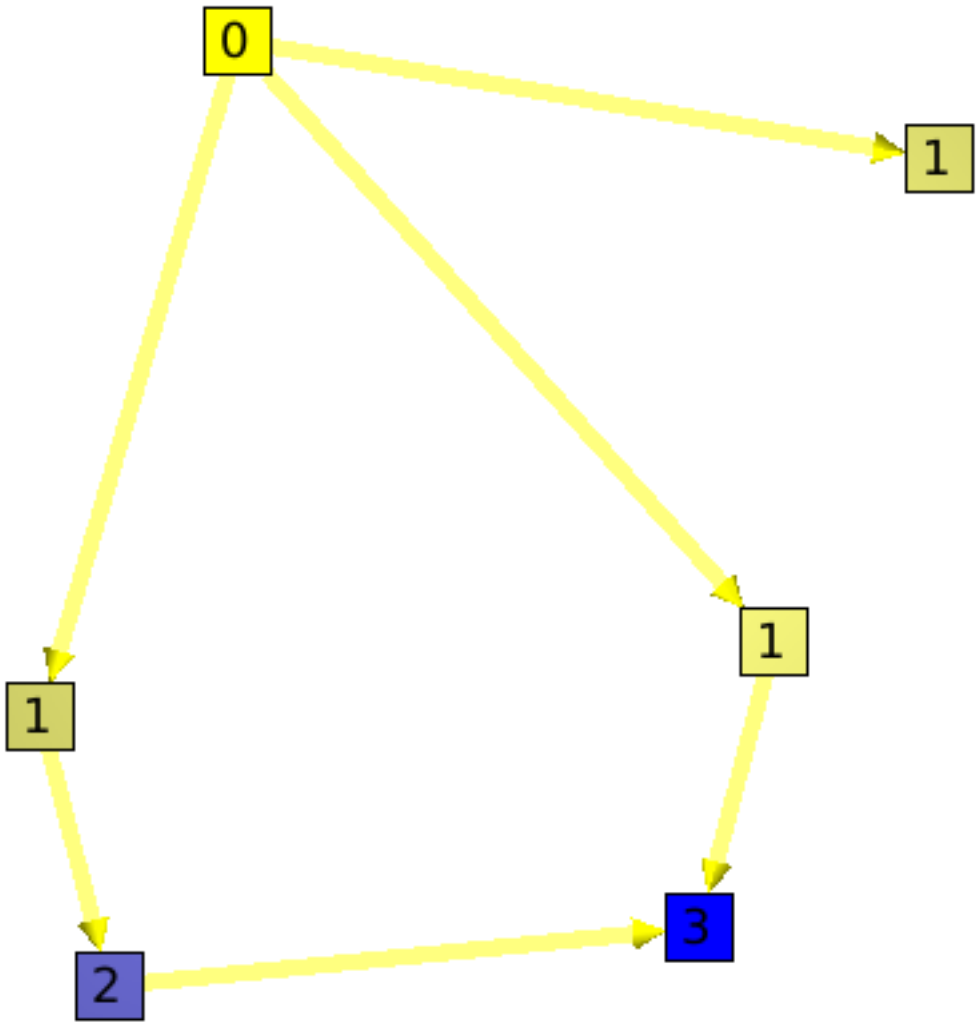


3.2.3.3. Tree

To use the following algorithms the graph has to be acyclic. A graph is acyclic if it contains no cycle.

3.2.3.3.1. Dag Level

The dag level algorithm will compute the depth of each node, as on the following example :



Algorithm documentation[20]

3.2.3.3.2. Depth

The depth algorithm will compute for each node, the maximum number of edges to follow to find a leaf.

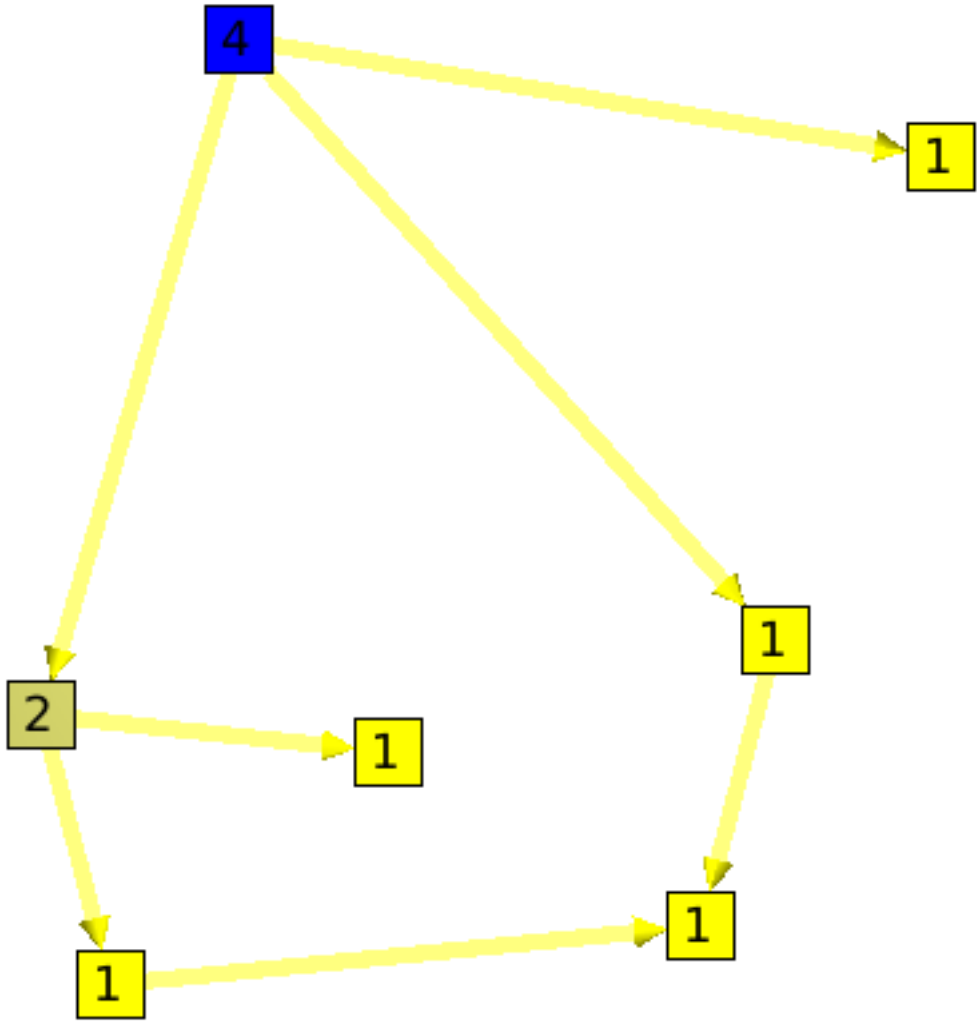
Algorithm documentation[21]

3.2.3.3.3. Leaf

The leaf algorithm will compute for each node its number of leaves.

Here is an example :

[20] ../../doxygen/allPlugins.html#DagLevelMetric
[21] ../../doxygen/allPlugins.html#DagLevelMetric



Algorithm documentation[22]

3.2.3.3.4. Node

The Node algorithm, will sum for each node the number of its children nodes plus him self.

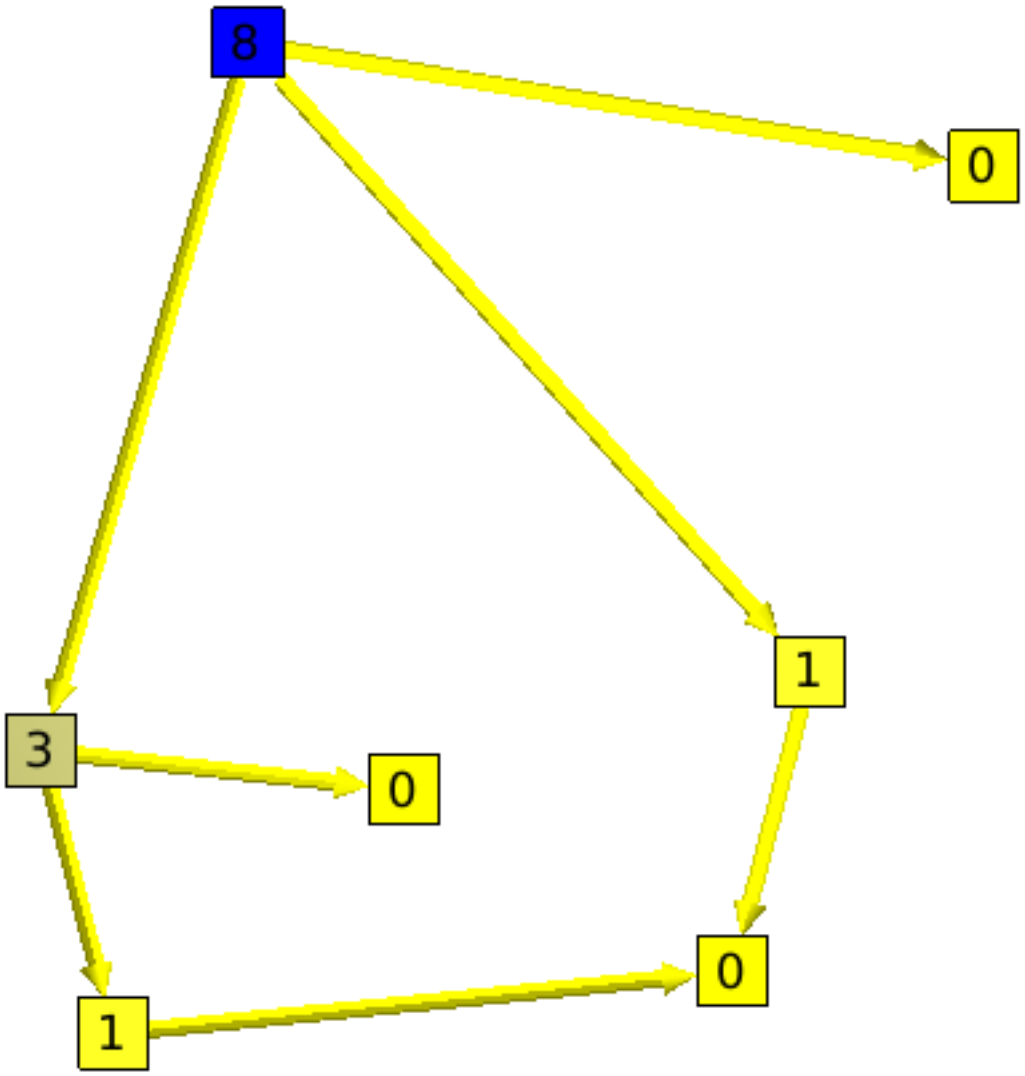
Algorithm documentation[23]

3.2.3.3.5. Path Length

This algorithm will count for each node the number of paths that goes through it.

Here is an example :

[22] ../../doxygen/allPlugins.html#LeafMetric
[23] ../../doxygen/allPlugins.html#NodeMetric

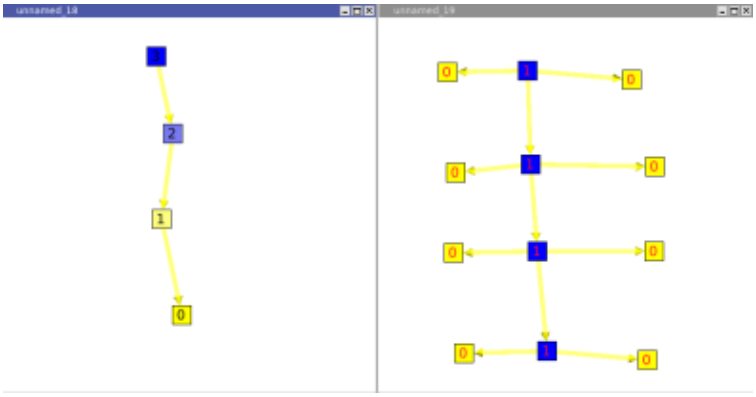


3.2.3.3.6. Segment

A segment, is a set of nodes that are all on one and only path. The graph showed on the left side of the example is a segment.

The segment algorithm will count, for all nodes, its number of edges without ramification.

Following are two graphs. On the left one you can see that the root "has" 3 edges without ramification. But, on the right graph all nodes (without considering leaves) have only 1 edge without ramification.



This algorithm can be useful to see how the graph is formed. Indeed, if the root has a small value, it will mean that the graph has a "good" ramification. But if the root has a high value, it will mean that the graph a lot of segments.

3.2.3.3.7. Tree Arity Max

Compute the maximum outdegree of the nodes in the subtree induced by each node. To access to the degree of a node it is recommended to use directly the degree function available in each Graph.
Algorithm documentation[24]

3.2.3.4. Misc

3.2.3.4.1. Id

The "id" algorithm will, for each node and edge, save their id number in their viewMetric Property. For example, if we have a node called Node 9, its id number will be 9.

Algorithm documentation[25]

3.2.3.4.2. Random

Random will just save a random number (from 0 to 1) in the viewMetric property of each node and edges

Algorithm documentation[26]

3.2.4. Layout

`Warning !` : Some of the following algorithm have no effect if the option "Force Ratio" is checked.

3.2.4.1. Planar

3.2.4.1.1. 3-Connected (Tutte)

This algorithm can only be applied to 3-connected graphs. A graph G is said to be 3-connected if there does not exist a set of 2 nodes whose removal disconnects the graph. (Triangle Layout)
Algorithm documentation[27]

3.2.4.1.2. Mixed Model

Create a planar sub-graph with polylines with a good angular resolution which will make the graph clear and easy to read.

Algorithm documentation[28]

3.2.4.2. Tree

[24] ../../doxygen/allPlugins.html#TreeArityMax
[25] ../../doxygen/allPlugins.html#IdMetric
[26] ../../doxygen/allPlugins.html#RandomMetric
[27] ../../doxygen/allPlugins.html#Tutte
[28] ../../doxygen/allPlugins.html#MixedModel

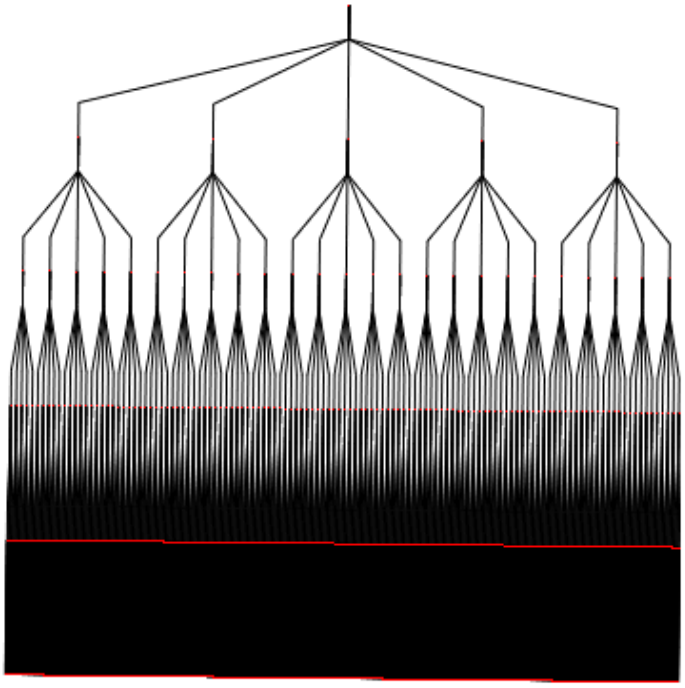
To represent a tree, a hierarchical layout is the easiest way to understand the tree structure. But this layout has a big weakness when the tree has a lot of nodes : it does not effectively use the space where the tree is displayed. That is why we need different layouts.

3.2.4.2.1. Bubble Tree

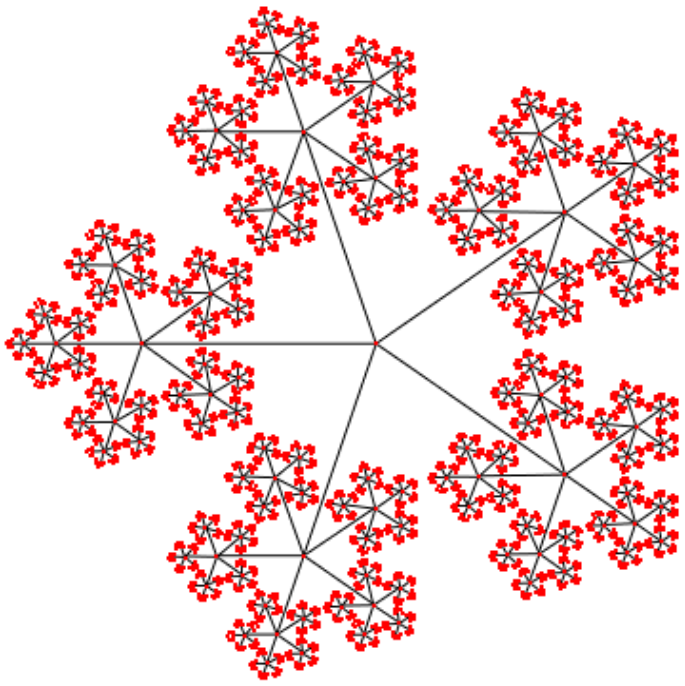
The Bubble Tree algorithm can be use to change the layout of a tree. On the new layout, a node will be on the center of a circle, and its children will be on the circle. This new layout has the following properties :

- The edges should not cross each other.
- The polyline used to draw an edge should have the least possible bends.
- The minimal angle between two adjacent edges of a node n should be nearest to 2pi / deg (n). This property will improve the angular resolution.
- The order of children of a node should be respected in the final drawing.

Here is an example :
The following graph has the default layout (hierarchical layout). It has a pretty bad angular resolution. Indeed, we do not see the leaves, but only a large black rectangle of edges.



Here is the same tree with a Bubble Tree layout. The angular resolution is much better.



Algorithm documentation[29]

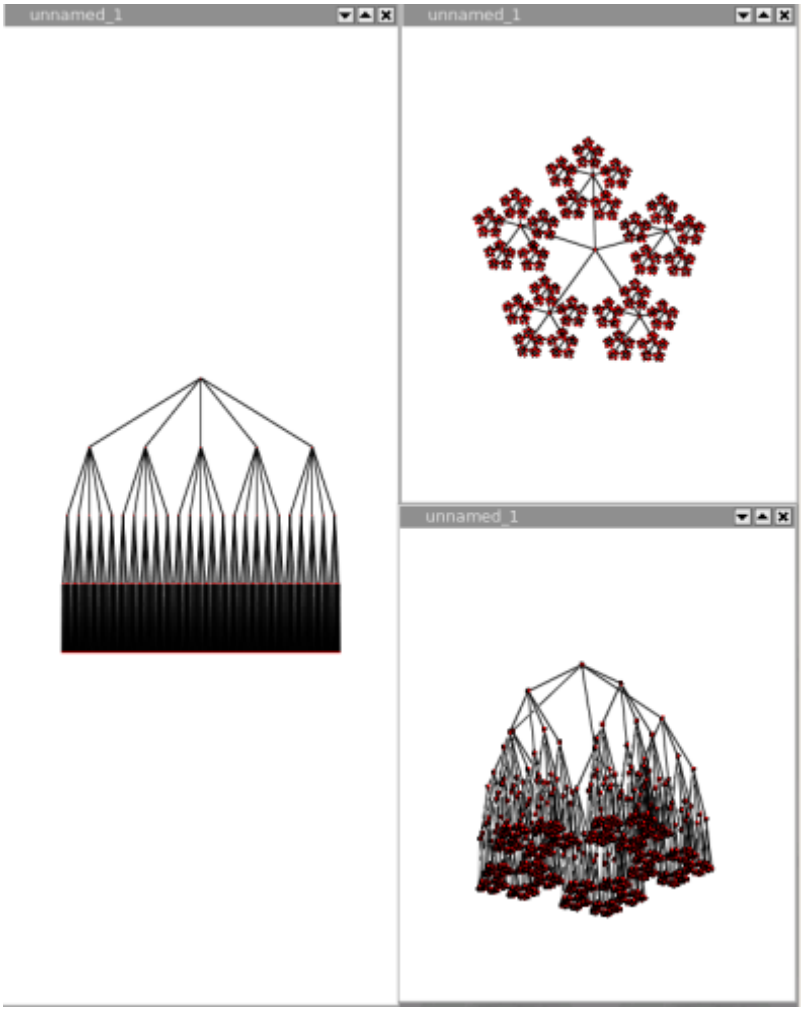
3.2.4.2.2. Cone Tree

The cone tree is a 3d layout which seen from the top, looks like a bubble tree. It takes two parameters:

- node size : size of the node will depend of the metric that you choose. The Algorithm will consider that parameter so that no nodes overlap themselves. This can be useful, if you want a node to be far from the others, just take a new size Metric and give a higher value to that specific node.
- Orientation : Vertical / Horizontal

Here is an example of this layout. On the left side you can see a tree with a hierarchical (classic) layout, and, on the right side, the same tree, but with a cone tree layout.

[29] ../../doxygen/allPlugins.html#BubbleTree



Algorithm documentation[30]

3.2.4.2.3. Dendrogram

The dendrogram layout is a hierarchical layout on which every leaves are displayed on the same layer.

A dendrogram is a tree diagram frequently used to illustrate the arrangement of the clusters produced by a clustering algorithm. Dendrograms are often used in computational biology to illustrate the clustering of genes.

The algorithm takes 4 parameters :

- node size : size of the node will depend of the metric that you choose. The Algorithm will consider that parameter so that no nodes overlap themselves. This can be useful, if you want a node to be far from the others, just take a new size Metric and give a higher value to that specific node.
- orientation : up to down, left to right, right to left or down to up.
- layer spacing : space between the levels of the Tree.
- node spacing : space between sibling nodes.

[30] ../../doxygen/allPlugins.html#ConeTreeExtended

Algorithm documentation[31]

3.2.4.2.4. Hierarchical Tree (R-T Extended)

The hierarchical tree layout looks the same that the dendrogram layout or the improved walker layout but takes an other parameter, "edge length".

- node size : size of the node will depend of the metric that you choose. The Algorithm will consider this parameter so that no nodes overlap themselves. This can be useful, if you want a node to be far from the others, just take a new size Metric and give a higher value to that specific node.
- edge length : this parameter can take a property of type int, and will be used to place a node on a specific layer. If its value is 1, no thing will happen, but if its value is 2, the node will be placed on the next layer.
- orientation : vertical/horizontal;
- orthogonal : enables the drawing of the edges, orthogonally bent.
- layer spacing : space between the levels of the Tree.
- node spacing : space between nodes sibling nodes.
- bounding circle : if checked, the estimation of overlapping nodes will be computed with bounding circles instead of bounding rectangles.

Algorithm documentation[32]

3.2.4.2.5. Improved Walker

The improved walker layout is just a hierarchical layout.
Algorithm documentation[33]

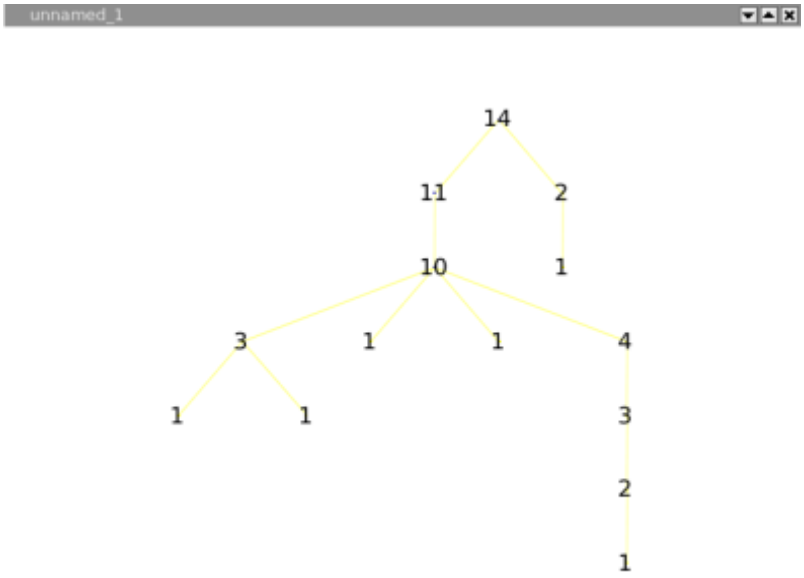
3.2.4.2.6. Squarified Tree Map

The squarified tree map layout, will place nodes in nested rectangles. For example, lets take a tree with a root and two sons, the layout will draw a rectangle for the root containing two other rectangles (its sons). This layout can be very useful for analyzing disks usages.

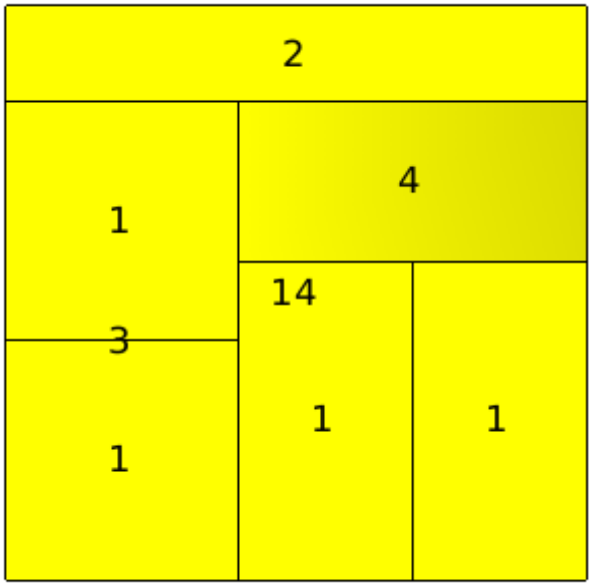
Here is an example :

Following is the tree a a file system containing 6 file of 1Mb, and severals directories.

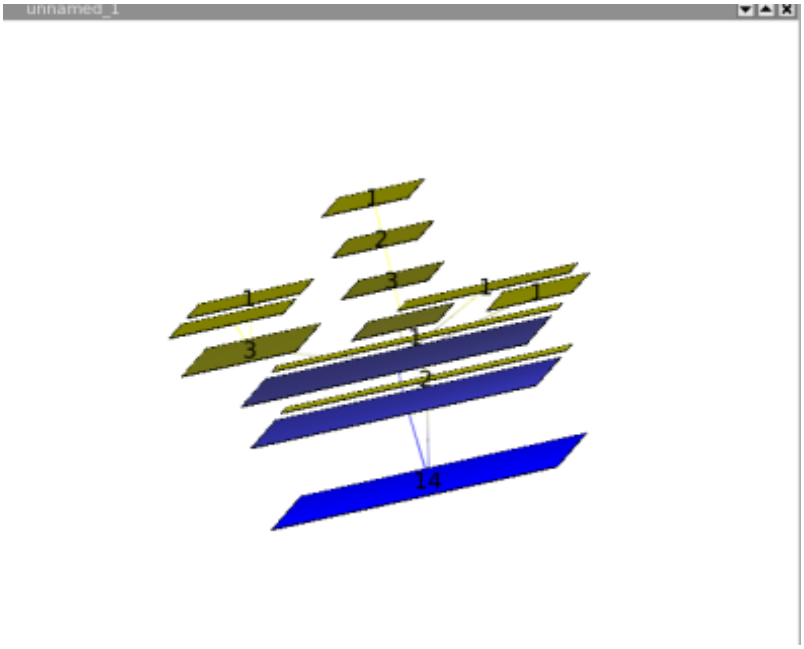
[31] ../../doxygen/allPlugins.html#Dendrogram
[32] ../../doxygen/allPlugins.html#TreeReingoldAndTilfordExtended
[33] ../../doxygen/allPlugins.html#ImprovedWalker



The same graph, with a squarified tree map layout :



Using the 3D, we can see how the layout is done :



Algorithm documentation[34]

3.2.4.2.7. Tree Leaf

This layout looks like the improved walker, but does not pack the nodes. The result is a nice hierarchical tree in which nodes does not overlap.
Algorithm documentation[35]

3.2.4.2.8. Tree Map (Shneiderman)

This layout, is the same as the squarified tree map layout, but the squarified tree map uses shadows to draw the tree.

Algorithm documentation[36]

3.2.4.2.9. Tree Radial

On this layout, nodes of the same layer are placed on a circle whose center is the root.
Algorithm documentation[37]

3.2.4.3. Basic

3.2.4.3.1. Circular

On this layout, every nodes are placed on a circle.

Algorithm documentation[38]

3.2.4.3.2. Random

Nodes are placed randomly in space.

3.2.4.4. Misc

3.2.4.4.1. Connected Component Packing

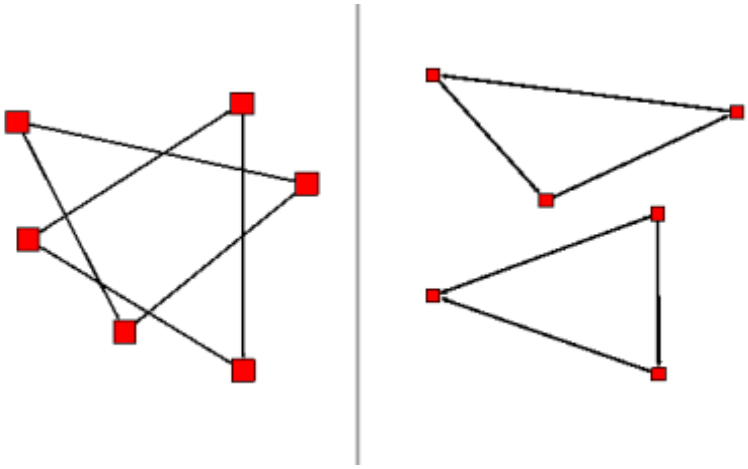
This layout groups connected components of the graph so that they do not overlap them-selves and that lost space is minimized (packing). It takes 4 parameters :

[34] ../../doxygen/allPlugins.html#SquarifiedTreeMap
[35] ../../doxygen/allPlugins.html#TreeLeaf
[36] ../../doxygen/allPlugins.html#TreeMap
[37] ../../doxygen/allPlugins.html#TreeRadial
[38] ../../doxygen/allPlugins.html#Circular

Functionalities

- node size : size of the node will depend of the metric that you choose. The Algorithm will consider that parameter so that no nodes overlap themselves. This can be useful, if you want a node to be far from the others, just take a new size Metric and give a higher value to that specific node.
- Rotation.
- Coordinates.
- Complexity.

Here is an example (left = before, right = after)

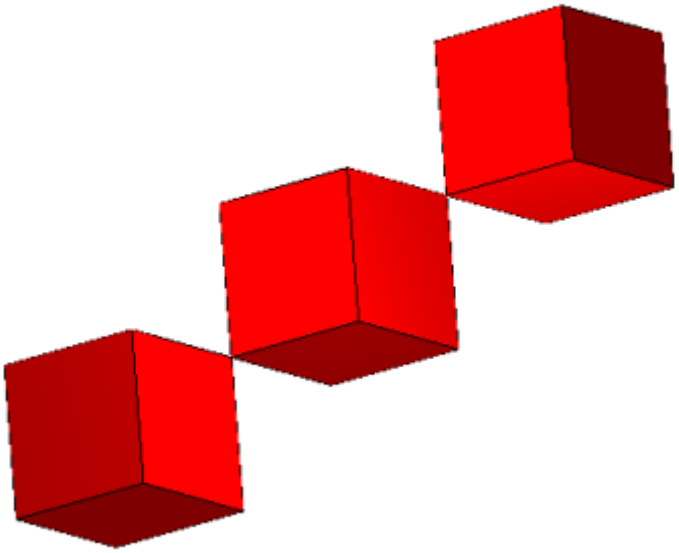


3.2.4.4.2. Scatter Plot

This layout can be used to see a correlation between 3 metrics (parameters). For example, if we have a node with "usedMetric1" = 0, "usedMetric2" = 1 and, "usedMetric3" = 2, the node will be place in the space with the coordinates : (0,1,2).

Following is an example, in which are 3 nodes. Those 3 nodes have 3 Metrics (called x,y,z). Node 1 equals to (0,0,0), Node 2 equals to (1,1,1) and Node 3 equals to (2,2,2).

We can see from the layout, that our correlation follow a linear function.



3.2.4.5. Force Directed

Force Directed layouts will try to place nodes so that, the distance in the graph (metric of the edges) should be the closest to the distance on the drawing.

`Warning !` : The previous property is not true at 100%.

3.2.4.5.1. Embedder (HDE)

The HDE layout, will only work on a 2D Mesh like graph.
Algorithm documentation[39]

3.2.4.5.2. GEM (Frick)

The GEM layout, unlike the HDE layout, works on all graphs. But it can take a very long computing time if the graph has more than 2000 nodes.
Algorithm documentation[40]

3.2.4.6. Hierarchical

3.2.4.6.1. Hierarchical Graph

This layout, will place the nodes of a graph as if the graph was a tree.
Algorithm documentation[41]

3.2.4.6.2. Hierarchical Graph 3D

This layout is the same that the "Hierarchical Graph" but in 3D.
Algorithm documentation[42]

[39] ../../doxygen/allPlugins.html#Embedder
[40] ../../doxygen/allPlugins.html#GEMLayout
[41] ../../doxygen/allPlugins.html#HierarchicalGraph
[42] ../../doxygen/allPlugins.html#GeneralGraph3D

3.2.5. Size

3.2.5.1. Auto Sizing

The auto sizing algorithm will resize nodes and edges of a graph so that the graph gets easy to read. The size of a node will depend on the number of its sons.

3.2.5.2. Fit to label

Fit to label, will resize nodes and edges so that labels fit in nodes.

3.2.5.3. Metric Mapping

The size of the nodes will change according to a metric.

3.2.6. General

3.2.6.1. Convolution

Convolution clustering is an approach to partitioning a graph that gives the user interactive control over how many clusters to create. Tulip calculates a density function based on the chosen metric, displays a convolution of its histogram, and partitions the graph according to the humps in the histogram.

3.2.6.2. Equal Value

This algorithm will create sub-graphs in which all nodes or all edges (not both a the same time), have the same value.

3.2.6.3. Hierarchical

This algorithm will divide the graph in 2 different subgraphs; the first one will contain nodes that have the viewMetric value under than a certain limit, and, the other one, in which nodes will have a the viewMetric value higher than the limit. Then, the algorithm will be re-applied to the subgraph (the one with higher viewMetrics) until the subgraph contains less than 10 nodes.
Algorithm documentation[43]

3.2.6.4. Quotient Clustering

This algorithm will create a metagraph. The metanodes, will be the subgraphs that already exist, and an edge will be created between two metanodes if and only if it exist an edge whose source is a node of a subgraph, and the target a node of an other subgraph.

Parameters :

- `oriented` : This parameter indicates whether the graph has to be considered as oriented or not.
- `node function` : This parameter enables to choose the function used to compute a measure value for a meta-node using the values of its underlying nodes.
- `edge function` : This parameter enables to choose the function used to compute a measure value for a meta-edge using the values of its underlying edges.
- `edge cardinality` : This parameter indicates whether the cardinality of the underlying edges of the meta-edges has to be computed or not. If yes, the property edgeCardinality will be created for the quotient graph.

[43] ../../doxygen/allPlugins.html#HierarchicalClustering

Functionalities

Algorithm documentation[44]

3.2.6.5. Strength

The strength algorithm will recursively create subgraphs that are nested "small-worlds".

Wikipedia: small worlds.[45]

Algorithm documentation[46]

3.3. Properties of graph

In Tulip, there is a way to assign properties to each node or edge of the graph. Tulip defines two kinds of property : intrinsic and extrinsic. The first represents the properties computed relatively to the structure of graphs. But it is possible to assign values to the nodes or the edges that are not related to the structure. For example, if we build the map of a region and the nodes represent the towns, the label property can be used for the name of town. But it is not possible to determine the name with the structure of the graph; this kind of property is extrinsic.

For each graph, Tulip provides a set of properties used by the renderer engine ; all begin with the “view” prefix by convention : viewColor, viewLabel, viewLayout... They are updated during the computation phase of the plugins. In the other hand, it is possible to define properties to store informations relative to the graph. The number of this created properties are not limited.

Following is the list of rendering properties :

- `viewBorderColor` : Color of the border of an edge or a node.
- `viewBorderWidth` : Width of the border of an edge or a node.
- `viewColor` : Color of an edge or a node.
- `viewLabel` : Label of an edge or a node.
- `viewLabelColor` : Color label of an edge or a node.
- `viewLabelPosition` : Label position (x,y,z) of an edge or a node.
- `viewLayout` : Position (x,y,z) of a node, or vector of the bends positions of the edges.
- `viewMetric` : Result value of the last measure (Section 3.2.3, “Measure”) algorithm applied.
- `viewRotation` : Rotation (0 to 360) of a node or an edge
- `viewSelection` : Selection equals true if the node or edge is selected. False if it is not.
- `viewShape` : Shape of a node or a graph.
- `viewSize` : Size (height, width, depth) of a node or an edge. To re-size an edge, the parameter "Size Interpolation" (CONTROL+R) must be switched off. For an edge, the three fields are : Width at source of the edge, Width at the end of the edge, Size of the arrow.
- `viewTexture` : Texture will replace the color background of the node.

[44] ../../doxygen/allPlugins.html#QuotientClustering
[45] http://en.wikipedia.org/wiki/Small-world_network
[46] ../../doxygen/allPlugins.html#StrengthClustering

3.3.2. Using Properties

3.3.2.1. Updates of property values

As it is explained in the last section, it is possible to update the properties attached to the graph elements with algorithms. An other solution is to update the values through the `Property` tab of the `Info Editor` subwindow.

To give an example, create a graph :

- Select the property you want to update, `viewSize` in the `local` table, for example, to manage the size of the nodes. Now, you can change all values or the value of one node.
  1. Click on `Set all`, and write the new coordinates : `(2.0, 2.0, 2.0)`
  2. Click on the line and the second column of the choosed node in the table. Change the values for the `width`, the `height` and `depth`.

If you want to change properties of selected elements, use the check box `selected only` of the `Property` tab.

- Select elements with the

  mouse toolbar operation or using the 'Add/Remove Selection' item displayed in the contextual pop-up menu which appears when pressing on the mouse right button (press **Ctrl** key when mouse pressing on Mac).

- Select the property you want to modify : `viewLabel`.
- Click on the checkbox named `Filter`. The selected element just appears in the table above.
- Click on `Set all` and write the text you want to display : "Hey!".

If you uncheck `selected only`, all nodes are in the table. It is possible to do the same thing with the values of edges. You just have to click on the tab named `Edges`. There is an other solution to modify the value of one node or edge :

- First select the

  mouse toolbar operation, then click on the node or edge you want to update.

- The `Element` tab of the `Info Editor` subwindow is then selected. It displays the informations of the element you clicked on.

3.3.2.2. Management of properties

The bottom of the `Property` subwindow enables to manage the properties. For each graph, as explain before, a set of display properties already exists. If you want to create a new property :

- Click on the `New` button.
- Select the type of property, `String`. (other possibilities are Color, Integer, Layout, Metric, Size, Selection)
- Type the name of the new Property (e.g. `mylabel`).

For removing a property, you just have to select the property and click on the button named `Remove`. When deleting properties used by the render engine, those properties will be temporary removed from the list but still continue to exist. Note that it is not possible to remove `inherited` properties.

The last feature is cloning property. Select the desired property and click on the button named `Clone`. Type the name you have chosen. The new property keeps the values.

3.3.2.3. Find : make a request.

The find tool is in the `Edit` menu. Make a graph with several nodes. Change some properties of node for making operations. Select nodes, check the `Filter` box and select the properties you want to change : `viewRotation`. Click on the `Set all` button and type a value (`20` for example). Now, you have some node with a rotation of 0 degree and some other rotated of 20. So in the Find box :

- Select the property used for the request : `viewRotation`.
- Choose the operation and type a value for the comparaisons : `=` and `20`, to find the element rotated of 20 degrees.
- Select the action in the `Options` part : `Add` and the kind of the elements of the request : `on nodes`.

3.4. Hierarchy

Tulip provides a system for the management of graphs hierarchies. The hierarchy sub-window displays the existing instances of subgraphs or groups with their relationships, the user can change the current view of the graph by clicking directly on the tree. When clicking the right mouse button, a pop-up menu is displayed, it allows to manage the instances of cluster : remove, clone, create subgraph.

3.4.1. Definitions :

3.4.1.1. Subgraphs :

A graph can have several parts of itself : these are stored in the subgraph instances. Some clustering algorithms can made subgraphs. A subgraph share its elements with the graph, it is just a part of the graph. It is possible to add properties for the subgraph only or to use the inherited properties.

For more information please visit : Wikipedia: Subgraphs [47]

3.4.1.2. Groups :

Some graph can be a subgraph of an other graph. This kind of hierarchy enables to assign a graph to a node.

3.4.1.3. Meta-graph :

A meta-graph is a graph that contains meta-nodes.

3.4.1.4. Meta-node :

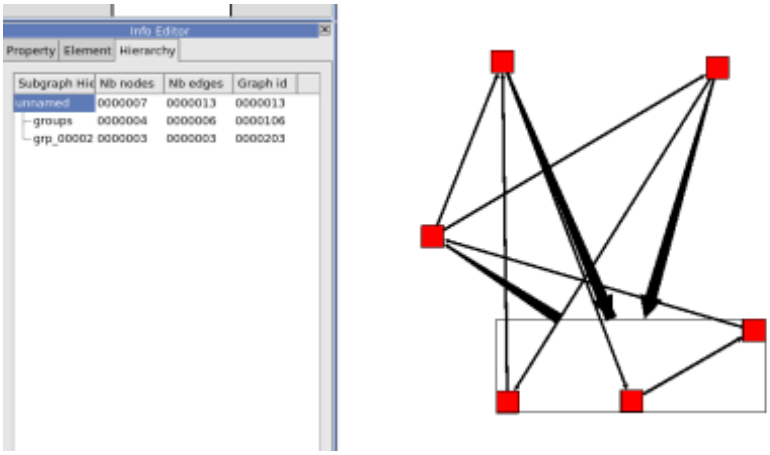
A meta-node, is a node that contain a group. A meta node can contain / refer to the root graph (Fractal effect).

3.4.1.5. Screen shots :

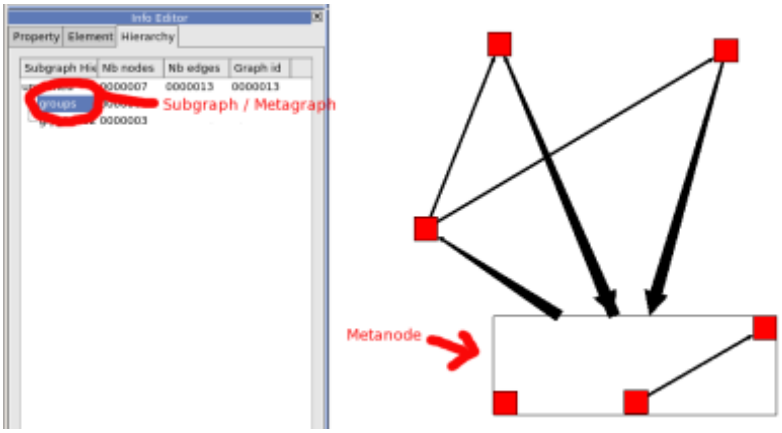
Following is an over view of a graph hierarchy :

The graph :

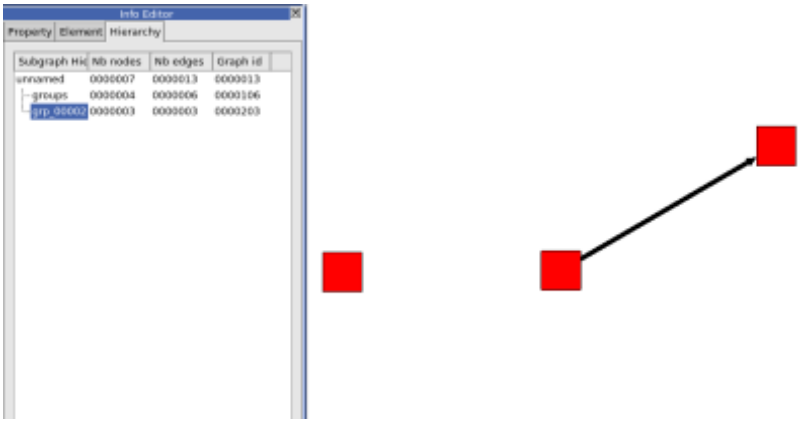
[47] http://en.wikipedia.org/wiki/Glossary_of_graph_theory#Subgraphs



The subgraph and the meta-node :



The group :



3.4.2. Creating subgraphs or Groups :

3.4.2.1. Creating a subgraph :

To create a subgraph follow these steps :

- `1 .` Select a few Nodes with the selection tool. (Shift + click, will add a node to the selection) To select the edges that are between the selected nodes use the "Induced Sub-graph" algorithm.

- `2 .` Create a subgraph : from the menu `Edit->Create Subgraph`, or from the keyboard, **Ctrl + Shift + G**. Give it a name.

You will be able to find your new subgraph in the hierarchy onglet of the info editor window.

3.4.2.2. Creating a group :

To create a group follow these steps :

- `1 .` Select a few Nodes with the selection tool. (Shift + click, will add a node to the selection) To select the edges that are between the selected nodes use the "Induced Sub-graph" algorithm.

- `2 .` Create a group : From the menu `Edit->Create group`, or from the keyboard **Control + G**. A warning saying "Grouping can not be done on the root graph a subgraph will be created" may pop up, if it does, just click `OK`.

You will be able to find your new group in the hierarchy onglet of the info editor window.

Severals subgraphs will be created :

- A copy of the root graph called "groups" containing a meta-graph with a new meta-node pointing to our group.

- A subgraph which is our new group.

3.4.3. Deleting / Ungrouping a subgraph or a Group :

3.4.3.1. Groups :

3.4.3.1.1. Delete .

To delete a group, left click on its name (in the Info editor) => delete

Note
By deleting a group, all nodes in this group will be deleted as well, whereas the meta-node will still exist.

3.4.3.1.2. Ungroup .

To ungroup a group, select it, Left click => Ungroup

Note
By ungrouping a group, all the layouts properties of the group's nodes will be applied to the root graph. The subgraphs created with the group wont be deleted.

3.4.3.2. Subgraphs :

To delete a subgraph, left click on its name (in the Info editor) => delete.

Note

Deleting a subgraph has no effects on the root graph.

3.4.4. Using subgraphs or groups :

3.4.4.1. Subgraphs

3.4.4.1.1. Moving a node in a subgraph.

If you move a node in a subgraph, the same node will be moved in the root graph.

3.4.4.1.2. Using an algorithm on a subgraph

If you use a layout algorithm on a subgraph, all changed layout properties will be applied to the root graph.

If you use a Measure algorithm on a subgraph, New local properties will be created. Those properties wont be applied to the root graphs.

3.4.4.2. Groups :

Changes on groups, wont be applied to the root graph unless you ungroup the group.

3.4.5. Algorithms that creates subgraphs :

You can find those algorithms in the menu Algorithm => General.

- Equal Value.Section 3.2.6.2, “Equal Value”
- Hierarchical.Section 3.2.6.3, “Hierarchical”
- Quotient Clustering.Section 3.2.6.4, “Quotient Clustering”
- Strenght.Section 3.2.6.5, “Strength”

3.5. Statistics Panel (not available in standard version)

Tulip also provides a simple statistics interface which allows the user to compute Histograms, Scatter Plots, Augmented Displays and Clustering. The computation of Histogram and Scatter Plot depends on a number for metrics, chosen by the user (from 1 to 3), and a discretization step (one given per metric). Finally, the clustering is performed from a clustering plane, specified by the user with a plane equation.

3.6. Text Rendering

It is possible to assign a label to each element of the graph. Tulip can display them with three methods : 3D and texture for node labels, bitmap for node and edge labels.

Figure 3.1. Bitmap Rendering

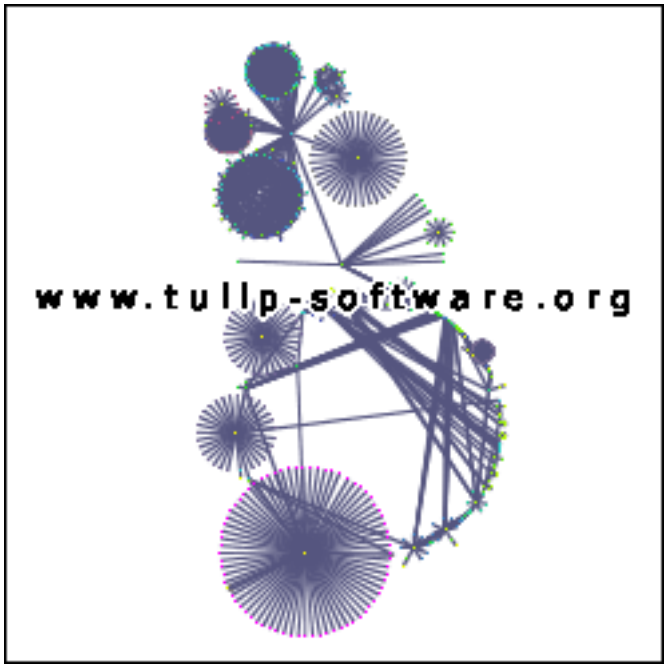


Figure 3.2. 3D Rendering

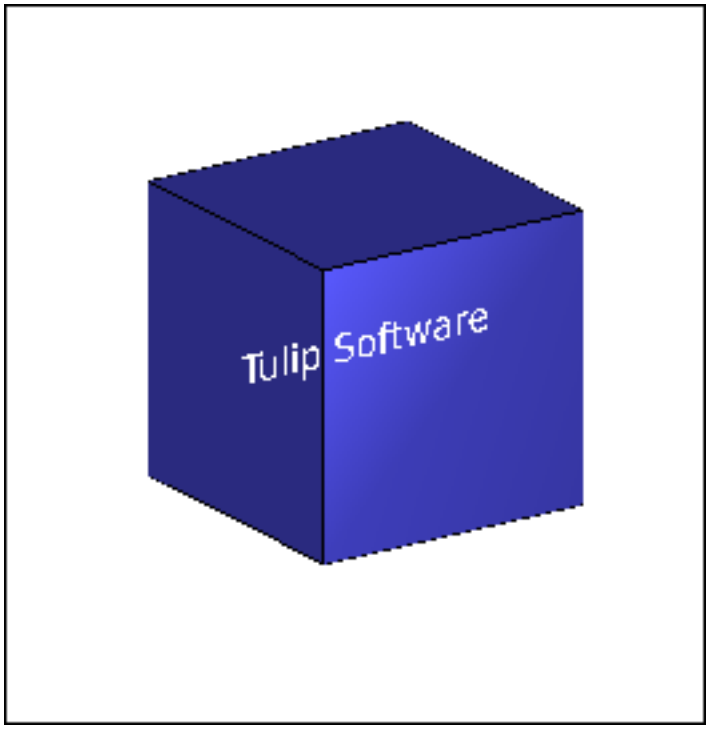
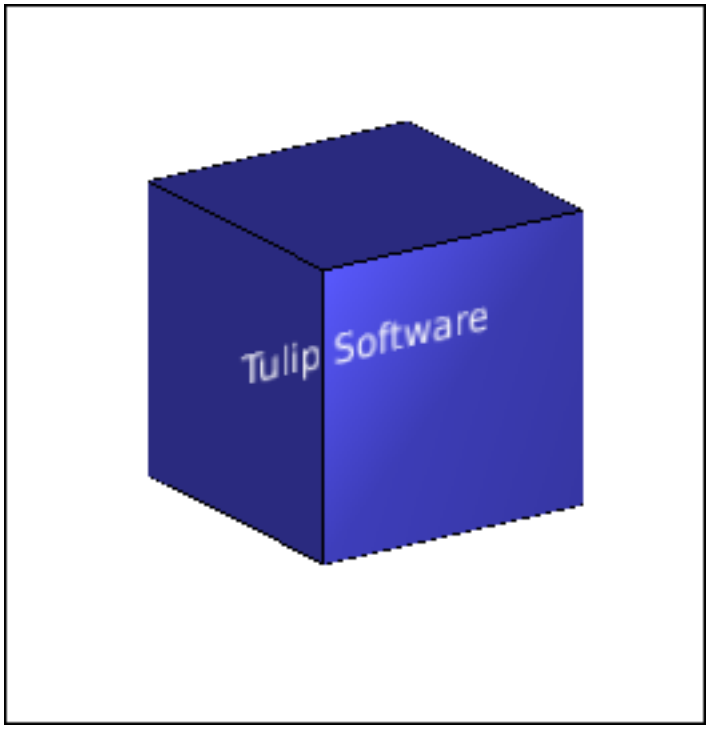


Figure 3.3. Texture Rendering



In a future version of Tulip, It will be possible to create labels with XML tags like the HTML rendering. Some tags will be available in order to allow the user to organize the content of the labels.

Chapter 4. Tutorials

4.1. First Step

In this part, the goal is to help you to simply make a graph and to save your work.

4.1.1. First graph display

4.1.1.1. Importation of a graph

- Select the `File->Import` item.
- Select a method of importation : `Grid approximation`, for example.

Do not modify the default parameters. Here is displayed the graph with nodes (red) and edges (black). With the wheel of the mouse, you can zoom on the graph to see a specific node. In moving the mouse with its left button pressed, you can translate the graph in the plane of the view, pressing the key **SHIFT** for rotation and the key **Ctrl** (**Alt** key on Mac) to rotate around the z axis and zoom. In order to come back to the oldest view, Select `View->Center view` from the menu bar.

- Select `Algorithm->Measure->Misc->Id` from the menu bar, to compute a value (metric) for each node and edge of the graph.

The graph is now displayed with colors depending of the metric. You can change the colors with the menu : `Algorithm->Color->Metric Mapping`. This plugin computes an interpolation between the two selected colors.

4.1.1.2. Creation of a graph

In this section, we learn how to create its own graph, element by element.

- Select the `File->New` from the menu bar to create a new graph.
- Create a graph adding nodes and edges. For a node, select the

mouse toolbar operation and click on the position you have chosen. To insert an edge, select the

mouse toolbar operation. Click on the source node, then on the target node. You can display or hide them with `Edges` checkbox in the `Overview` subwindow. In the same way, you can display or hide the arrows checking `Arrows`.

- Delete elements of the graph. Select the

mouse toolbar operation, then click on the element you want to delete.

4.1.2. Save options

To save your work, you just have to select `File->Save` or `Save as`: a dialog appears allowing to enter the author of the graph and some comments; then after clicking on the 'OK' button, just type the file name and choose its location.

The second way to make a save is to export the graph in a special format : GML or TLP (equivalent to `Save as`). Select `File->Export` and the format of your choice, then choose the file name and location.

4.1.3. Algorithms

This part explains how to apply an algorithm to a graph. Previously, you have created or imported a graph. Select `Algorithm->Layout` (for example) and an algorithm : `Hierarchical->Hierarchical Graph` for example.

In this case, we use an algorithm dealing with the layout of the nodes and the edges. It is possible to apply all other kinds of algorithm. Some `layout` algorithms may not apply to your graph if it does not belong to the right category of graphs. With the `Bubble Tree` layout, you can not display a grid. If it is not valid, a pop-up message will displayed explaining the problem.

4.2. Improving a layout

4.2.1. Introduction

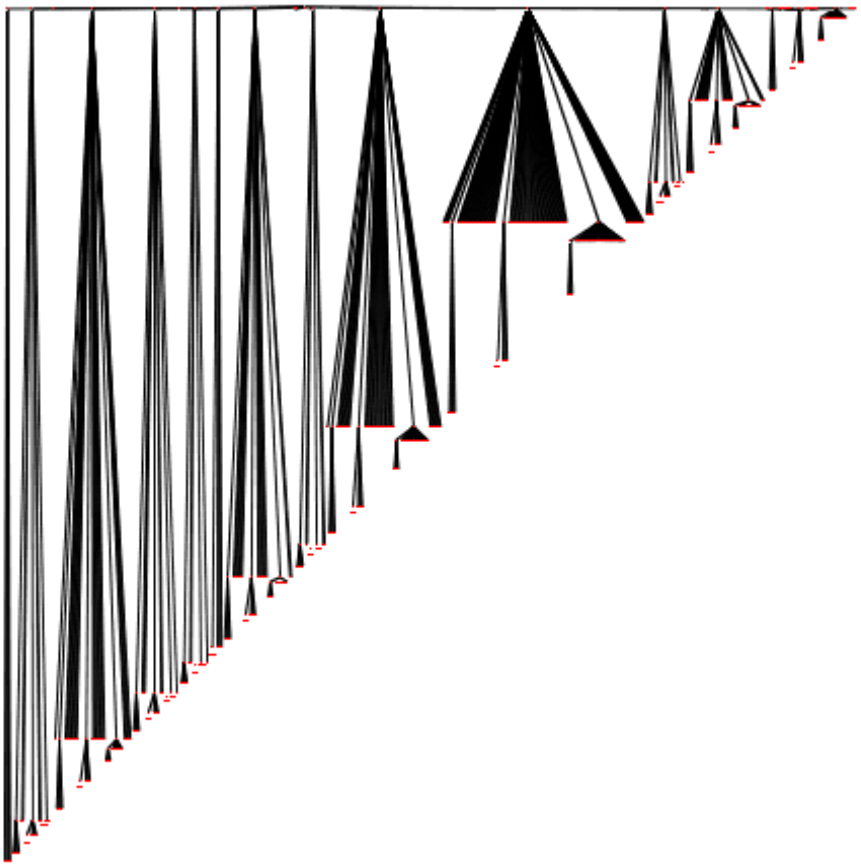
In this tutorial, we will show you how to use, layouts algorithms, and graph properties to obtain a nice an clear graph. To do so, we will first import a file-system structure, and then use the graph properties to find specific files. (*.cpp or *.hpp ...)

4.2.2. File-system importation

To import a file-system we need to select the `File System Directory` importation tool which is in the menu `File->Import->Misc`.

A "file browser dialog" will pop-up to select the root directory that you want. On this dialog, you just need to select a directory for instance, your documents (On Windows : My Documents).

The importation plug in will work for some time, and a tree graph will appear representing the file system chosen.



To follow the rest of this tutorial you need to download this tulip graph file : Graph[1]. Load this compressed tulip file into the software (`File->Open`).

4.2.3. Using other Layouts :

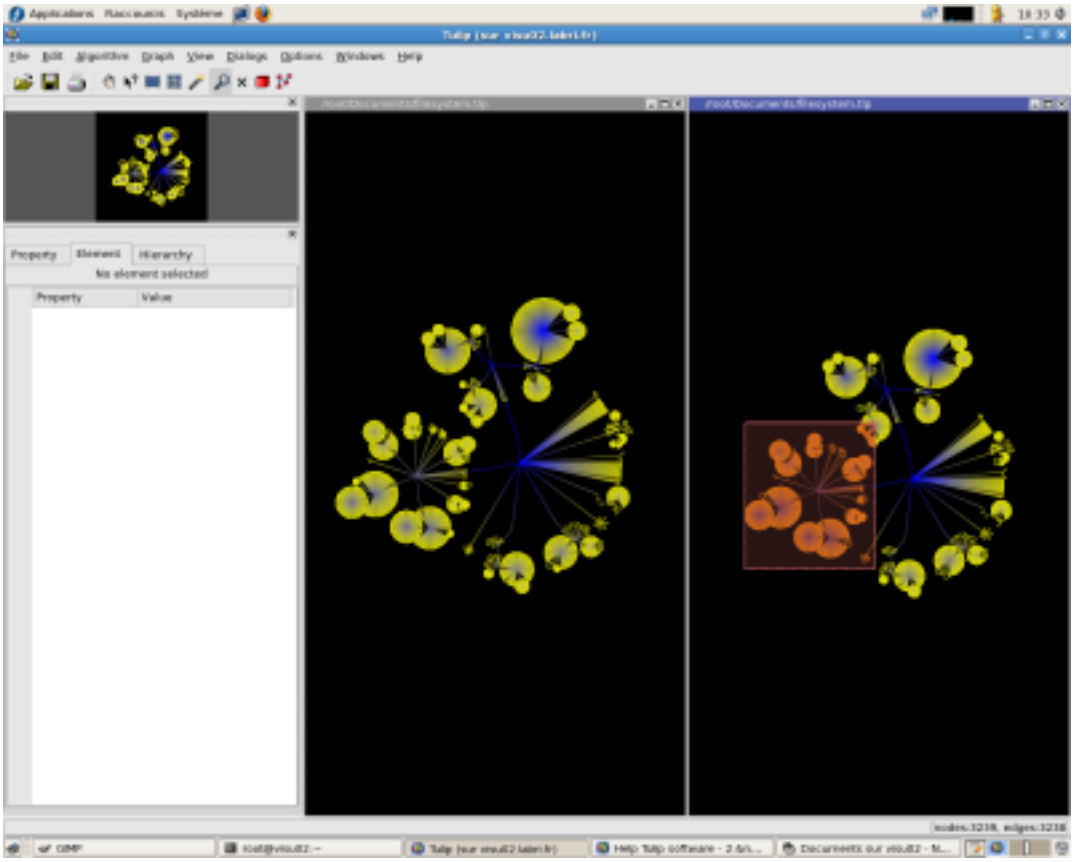
4.2.3.1. `Bubble Tree Layout` :

This layout algorithm can be found in the menu `Algorithm->Layout->Tree`. The bubble tree layout is very useful to notice directories that have the same structure. In this section, we will try to locate those directories.

To have a better view on the tree, we will create a new 3D view. Menu : View->New 3D view or press **Ctrl+Shift+N**. When the new view is created, we need to re-organize the windows. Menu : Windows->Tile.

Now that we can see the both views at the same time, we will zoom in (right window). Select the magnifying glass tool, and draw a bounding box on the left side of the graph. Just like this :

[1] http://www.labri.fr/perso/auber/projects/tulip/samples/filesystem.tlp.gz



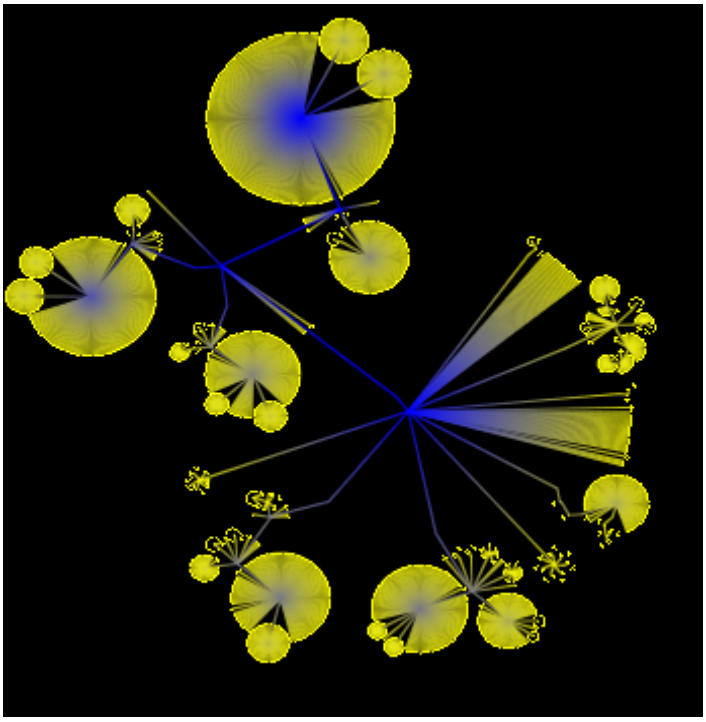
As you can see, two nodes looks very alike. By using the "Get Information " tool, we can get there ids : Node 1965 and node 2009. Indeed, those to directories have the same structure since they both contains plug-ins source files.

We will now re-center the view (`View->Center View` or **Ctrl+Shift+C**).

Let's say that we now want to study our graph without the plug-in directory. To delete it we have first to select it, and then select all its sub directories.

- Select the plug-in directory : Use the Find tool, (`Edit->Find` or **Ctrl+F**) with the field `Input property` set to "name", filter function set to "=" and filter value set to "plugins".
- Select all its sub-directories : Use the `Algorithm->Selection->Reachable Sub-Graph` algorithm with the field distance set to 50.
- Delete all the selection : press **Del**
- Re-draw the bubble layout `Algorithm->Layout->Tree->Bubble Tree`.

Following is what you should see :



As you can see, the bubble tree layout can be quite useful.

4.2.3.2. The Tree Map layout :

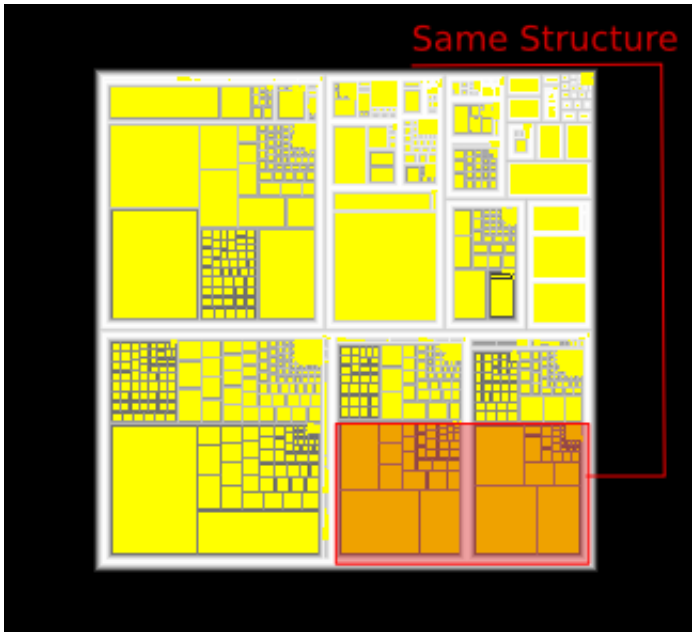
This Layout algorithm can be found in the menu `Algorithm->Layout->Tree`. The treemap layout is very useful to notice large disk usage files. This section will show you how to use the tree map layout

First, make sure that you have unchecked the `Force Ratio` option that you can access via the menu `Options`.

Apply the layout algorithm `Algorithm->Layout->Tree->Squarified Tree Map` with the following parameters :

- Metric : set to "size".
- Aspect Ratio : set to 1
- Texture? : checked

Do not forget to refresh the views (**Ctrl+Shift+R**). Following is what you should see :



As you can see, we easily get a global information on the size of files. Which is the biggest, or, which is the smallest ? But, we can also see the structure of directories, since files and directories are nested nodes. See Wikipedia : Tree Maps [2] for more information.
An other layout can be useful, the Improved Walker.

4.2.3.3. `Improved Walker layout :`

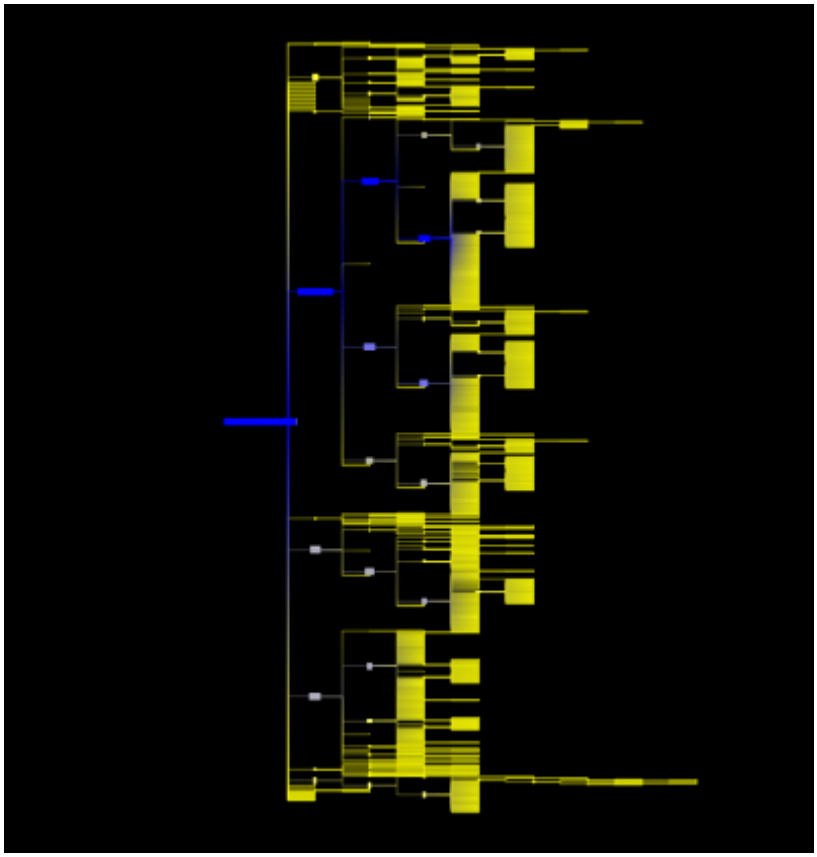
This layout can be find in the `Algorithm->Layout->Tree->Improve Walker`.

Use the following parameters :

- Node Size : viewSize
- Orientation : Left to right.
- Orthogonal : Checked.
- Layer Spacing : Default value.
- Node Spacing : Default Value.

You should see a tree looking like this :

[2] http://en.wikipedia.org/wiki/Tree_map



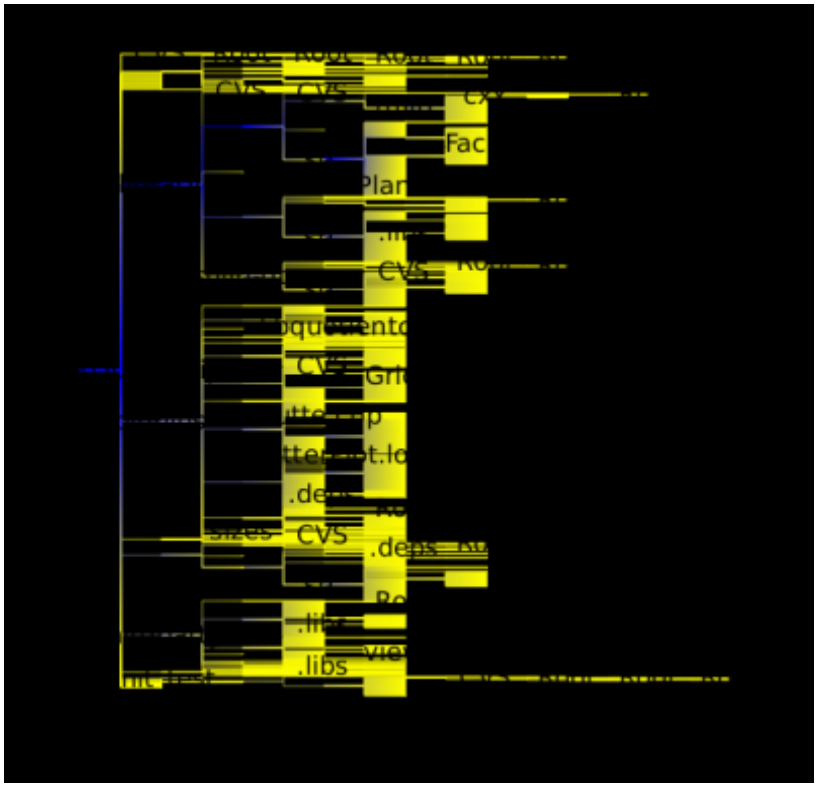
As you can see, the improve walker layout, is just a hierarchical layout. It is very useful to understand the tree structure of a file system.

4.2.4. Showing Labels

First, in the `Rendering Parameters` dialog (**Ctrl+R**), check the `nodes` box for the `Visibility` option.

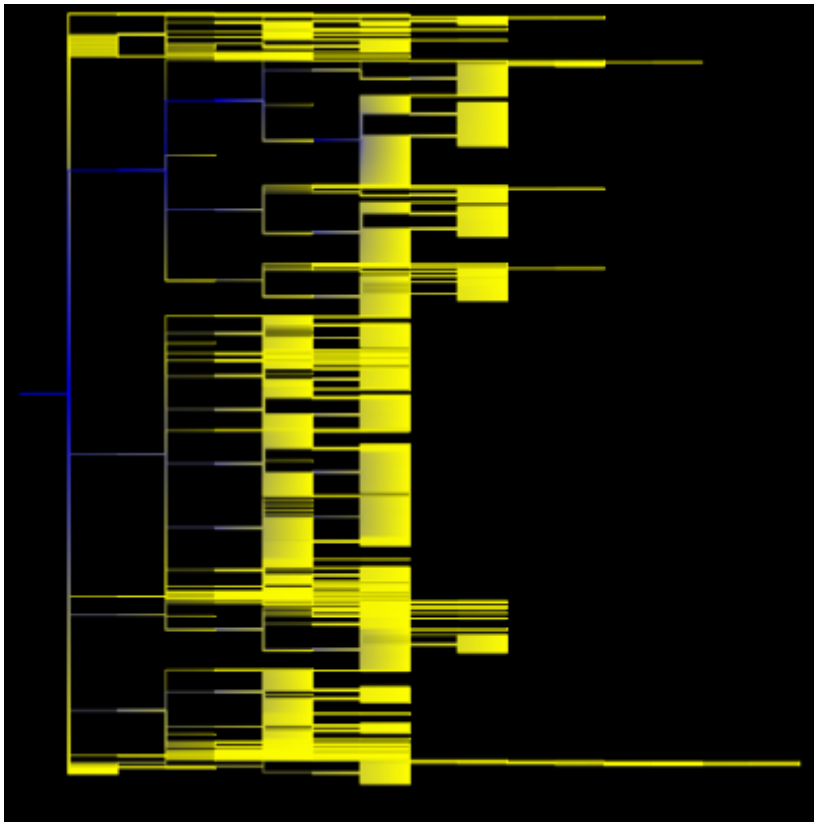
We will now try to add labels to the nodes. To do so, select the node property called "name" in the info editor window, click on the button `To Labels`.

You should now see a graph looking like that :

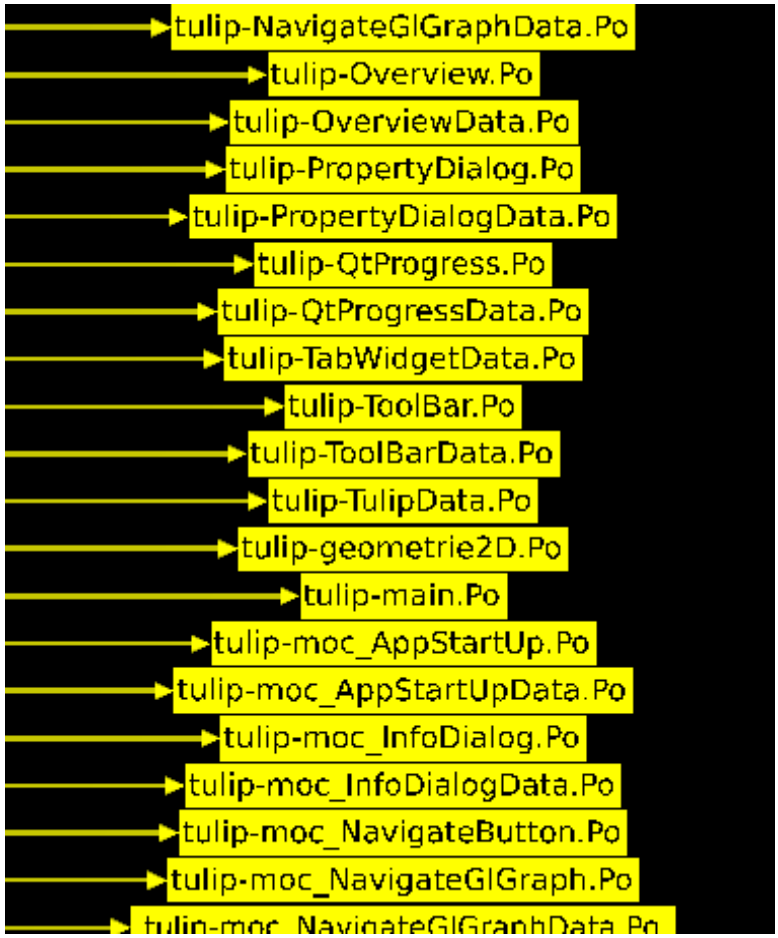


As you can see, the labels, don't fit in nodes and it is very hard to read the graph. To fix this problem, press **Ctrl+R** , in the Labels box, the field `Type` must be equal to "3D". Then, apply the `Algorithm->Size->Fit To Label` algorithm.

You should obtain something like this.



By zooming in we can see the labels :



If you want to display the big file (high disc space) with big nodes, use the `Algorithm->Size->Metric Mapping` algorithm with the parameter called "property" set to "size".

4.2.5. Showing a specific kind of file.

Now that our graph as a nice and clear layout, we would like to locate all of our Source files (*.cpp). To do so, we will use the Find tool (Edit->Find or **Ctrl+F**).

Use the following parameters :

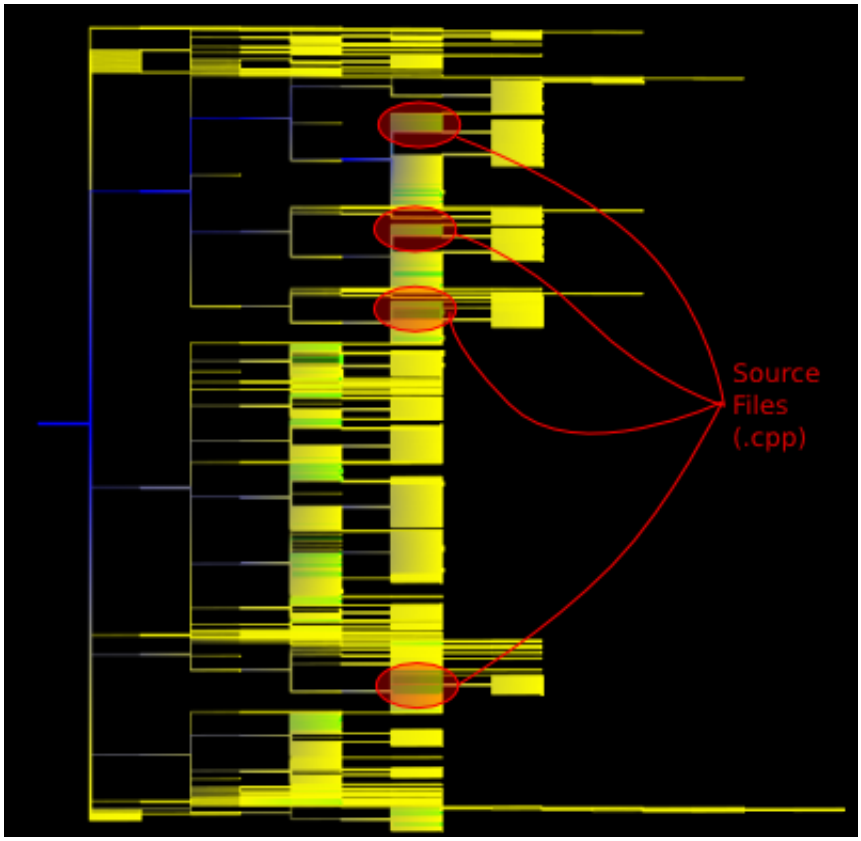
- Input Property : name
- Filter : filter function set to "=" and filter value set to ".*cpp or .*hpp". For more details on regular expressions, follow this link : WikiPedia : Regex [3]
- Options : check the `Replace` radio button and select `On nodes`.

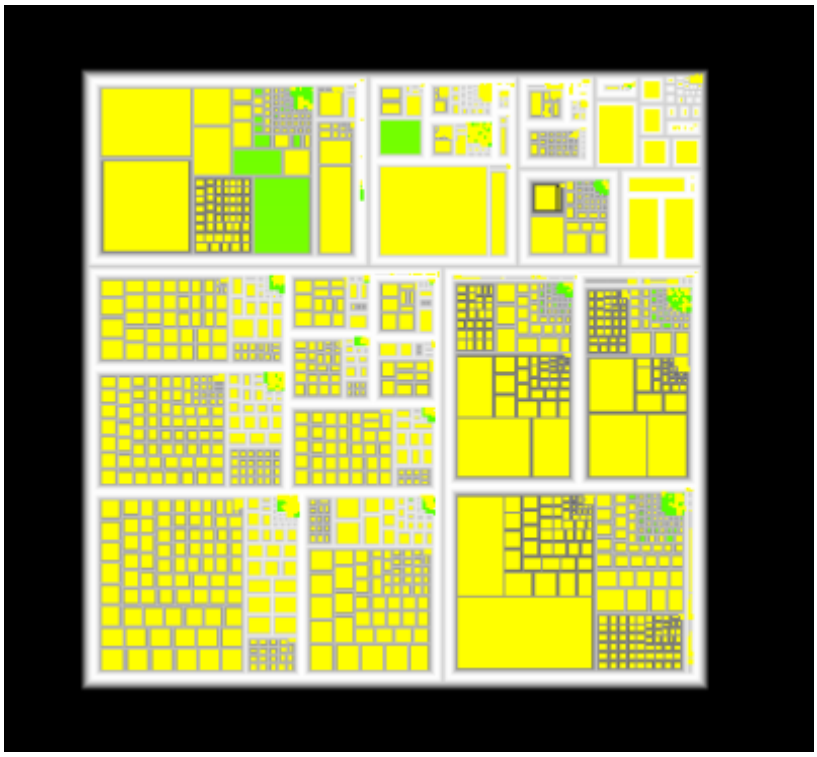
Now that our source files are selected, we will apply a different color to them.

In the info editor window, select the node property called "viewColor", check the `selected only` option. Now that we only see the "viewColor" property of the selected nodes, click on the button `Set all` and choose the color that you want. (We choosed green)

You should see a graph like the one following :

[3] http://en.wikipedia.org/wiki/Regular_expression





4.2.6. Conclusion

As you could have seen, tulip implements powerful layouts and tools, to make a simple and understandable graph from a complex one.

4.3. People in InfoVis

4.3.1. Analyzing an author.

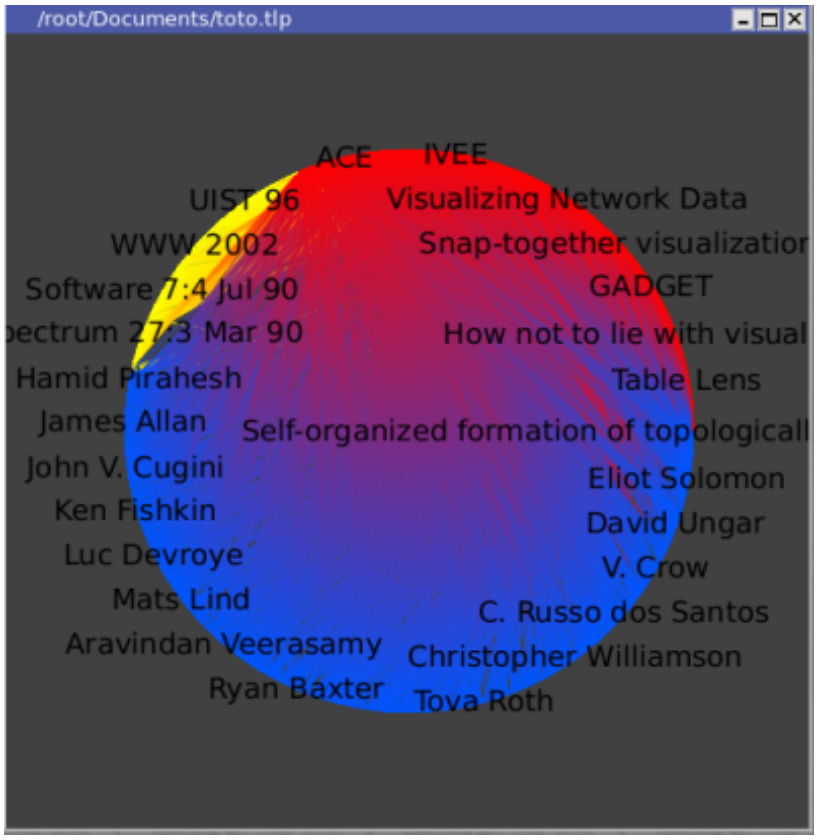
Before anything, download, and open this tulip graph file[4]. Click on the tab Hierarchy (in the info editor window) and select the subgraph GRCite. You need to delete the other sub graphs by doing a right click on there name, and then "remove".

This graph represent the relations between authors, conferences and papers. To distinguish paper, conferences and authors, we will re-color them :

- Select all papers : Press on **Ctrl+F** to display the find tool. In the Input Property field, select the property "type". And on the line below, set the filter function to "=" and the filter value to 0, before clicking on the Find button.
- Re-color the nodes in red : Select the tab Property (in the info editor). Check the "selected only" option. Select the property viewColor, and, by clicking on the button "Set all" choose the red color.

Repeat the actions above, for authors (type = 2) and conferences (type = 1) with other color (blue , yellow).

You should obtain something like this :

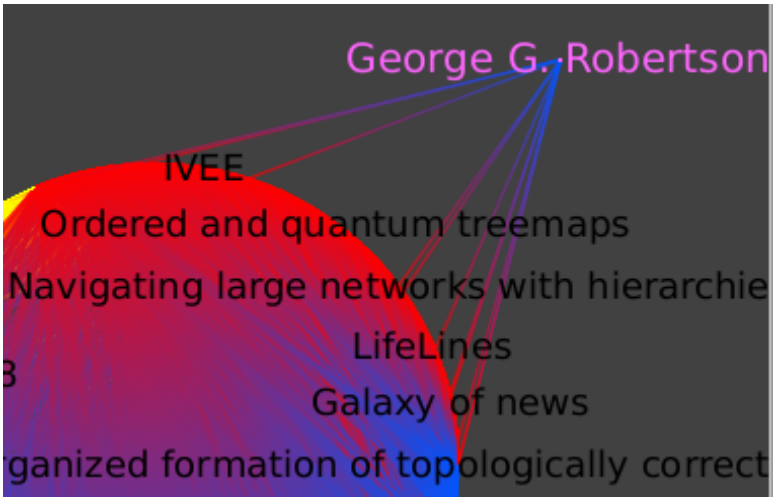


`Select an author :`

Let's pick a single author to investigate, in this case George Robertson. First, we interactively select that node by hitting **Ctrl+F** for the find tool, choosing the "titleshort" property, the "=" as filter fuction, and the regular expression "G.*Rob.*" as filter value. We then quickly check to see how he is connected to the entire graph by temporarily moving that node away from the others to see roughly how many edges are attached to it.

Following is what you should get :

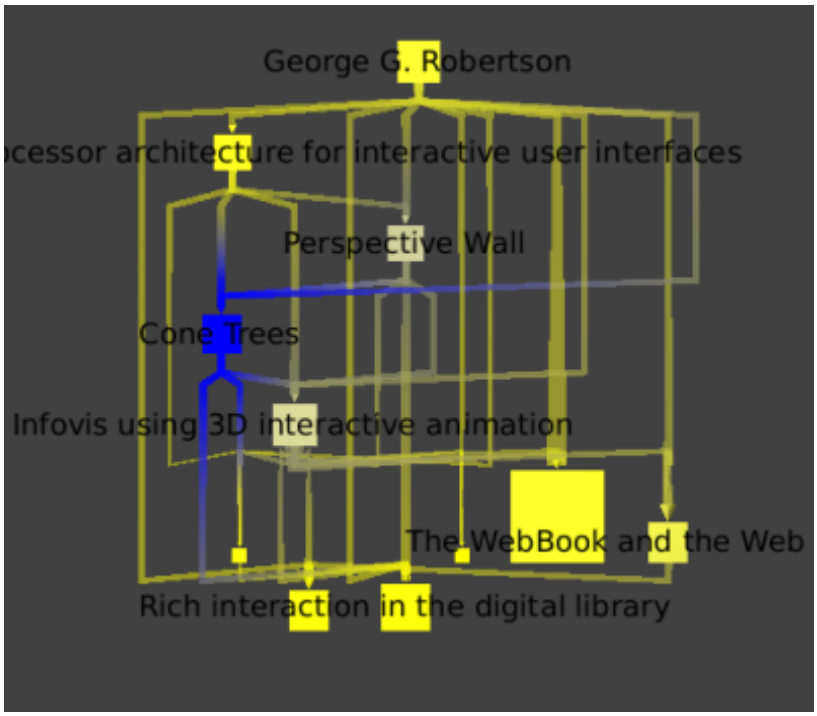
[4] http://tulip.labri.fr/samples/GRCite.tlp.gz



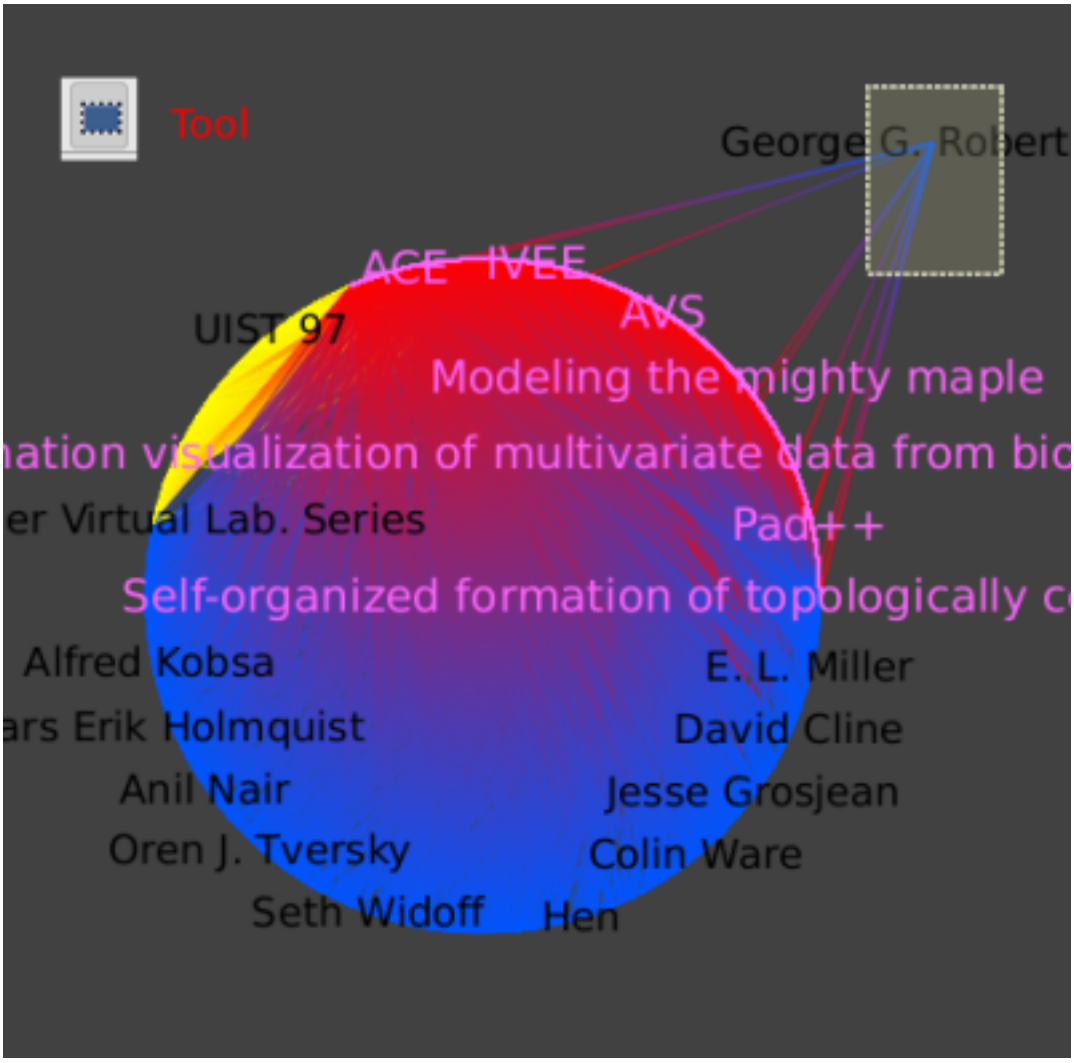
`Go deeper :`

We then select the menu item `Algorithm->Selection->Reachable Sub-Graph`, type 1 for the distance into the popup panel and 0 for the direction of the edges (outgoing). We then select the menu item Edit->Create Subgraph to save this selection for further manipulation, naming it GR.1hop.outgoing. We then select this new subgraph in the hierarchy tab, and lay out this subgraph using a hierarchical drawing algorithm (`Algorithm->Layout->Hierarchical->Hierarchical graph`).

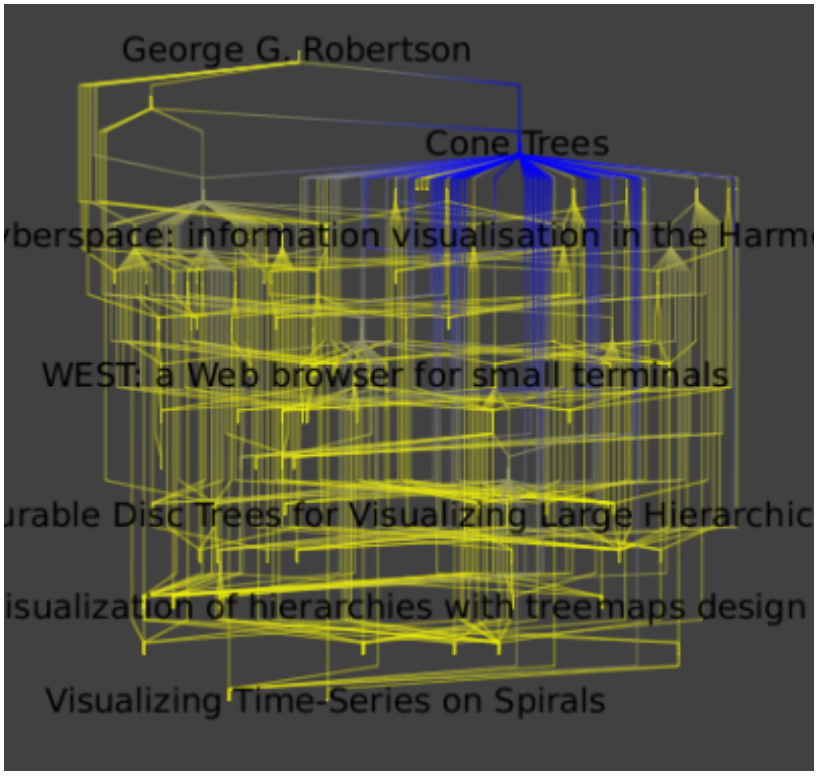
We can see simply from the drawing which papers were published first, as they are cited by the later ones. Robertson has published 11 papers in this database. The coloring by the number of citations (`Algorithm->Color->Metric Mapping`, with field property set to "arityOut") shows that "Cone Trees" is his most influential work.


George G. Robertson
cessor architecture for interactive user interfaces
Perspective Wall
Cone Trees
Infovis using 3D interactive animation
The WebBook and the Web
Rich interaction in the digital library

Finally, we select all papers by hitting **Ctrl+F** for the find tool, choosing the type property, the "=" filter, and the value 0 for papers. We explicitly add Robertson to the selection using the selection tool to select its edges too (see below), and save this whole set to a new subgraph that we name GRCitesub:



In the new subgraph, we then select the Robertson node. Again as above, use the `Algorithm->Selection->Reachable Sub-Graph` algorithm, pick a depth of 2 to find all papers that cite a paper written by Robertson, and save the resulting subgraph using the Edit->Create Subgraph menu. The final image shows the result of using the `Algorithm->Layout->Hierarchical Graph` layout.


George G. Robertson
Cone Trees
berspace: information visualisation in the Harm
WEST: a Web browser for small terminals
rable Disc Trees for Visualizing Large Hierarchic
isualization of hierarchies with treemaps design
Visualizing Time-Series on Spirals

You can now close this graph since we are going to use an other one for the following of this tutorial. The next graph is similar to the this one but, has coauthorship edges linking authors who write papers together. You can download it[5] and open it in tulip.

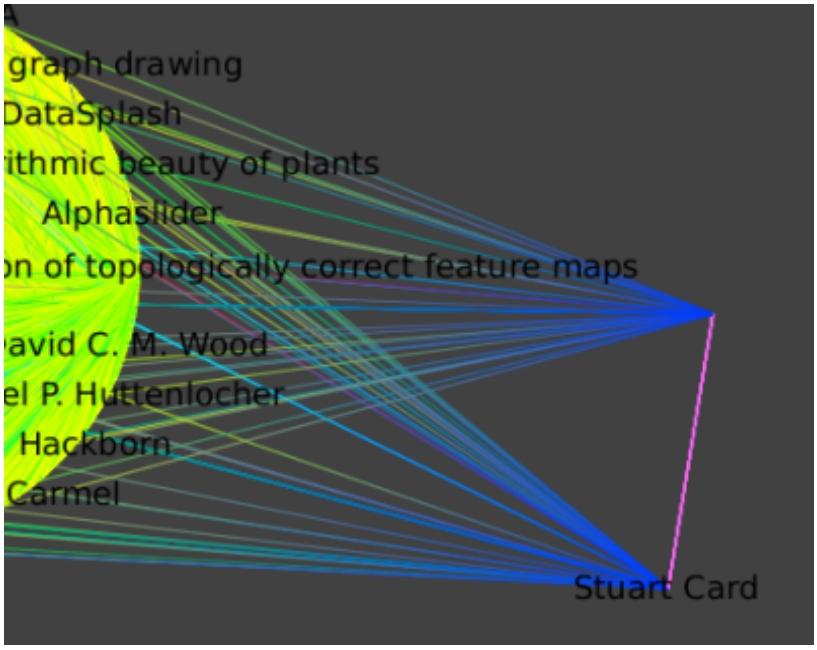
4.3.2. What, if any, are the relationships between two or more or all researchers

4.3.2.1. Focusing on Two Authors

Here we focus on the relationship between two authors, in this case Robertson and Card.

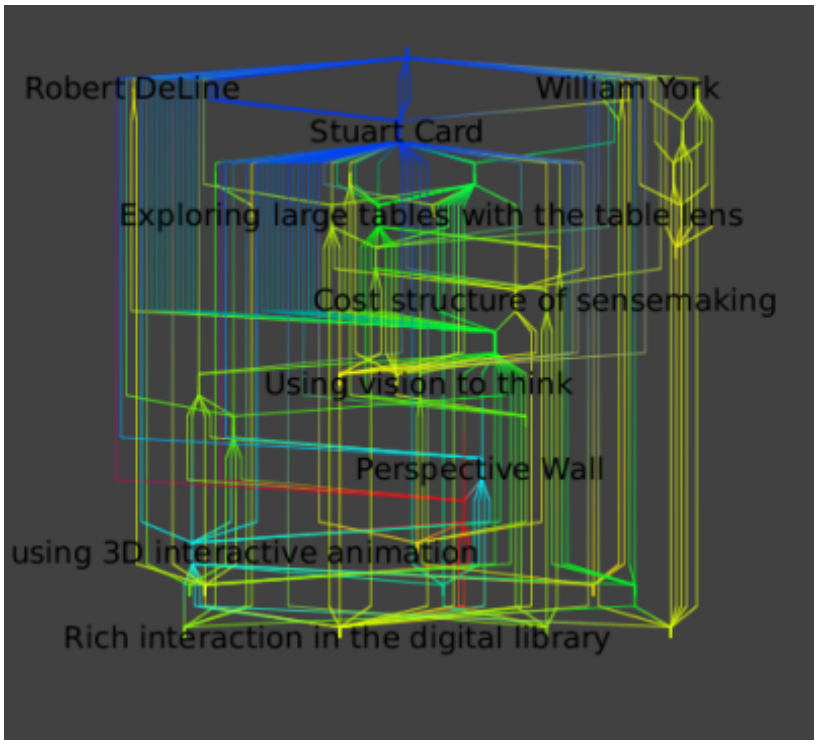
To select them use the find tool, with, at the first time the regular expressions : "G.*Rob.*". And at a second time, the regular expression ".*Card.*" and the "add" option checked. To move those selected nodes away from the main layout, use the "moving selection" tool. If you click on one of the node, you will be able to move both nodes at the same time.

[5] http://tulip.labri.fr/samples/GRSC.tlp.gz

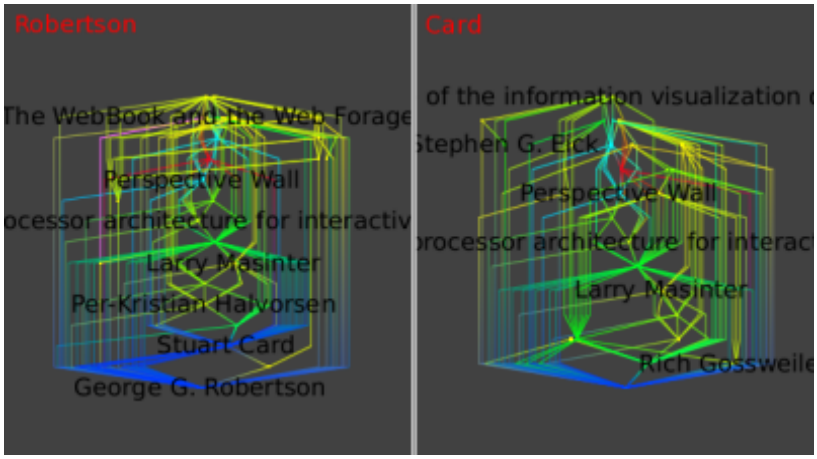


Select Card and Roberts at the same time (Press **Shift** while clicking on a node). Select all their neighbors by applying the `Algorithm->Selection->Reachable Sub-Graph` algorithm with distance 1. Create a new Subgraph.

Following is a hierarchical layout of the neighborhood of all outgoing edges one hop away; that is, the publications and coauthors of the union of Card and Robertson.



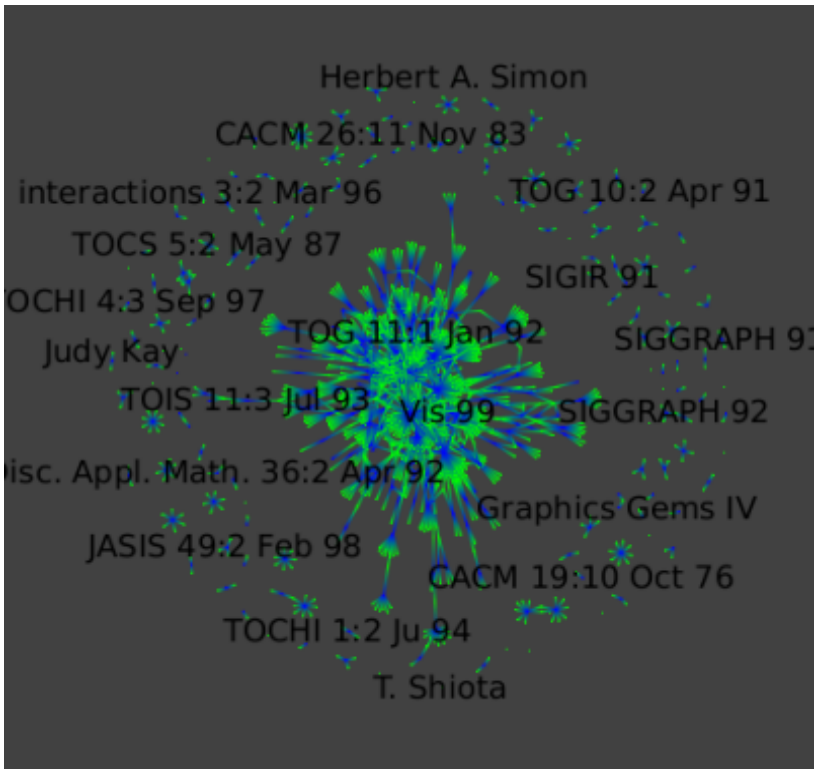
You can repeat those operations for Robertson only and Card only :



The similarity of these final three images shows the very strong ties between these two authors.
You can now close this graph since we are going to use an other one for the following of this tutorial. The next graph is similar to the old one but, has links between author and conference by following links from author to paper, and from paper to conference. Then, delete papers. You can download it[6] and open it in tulip.

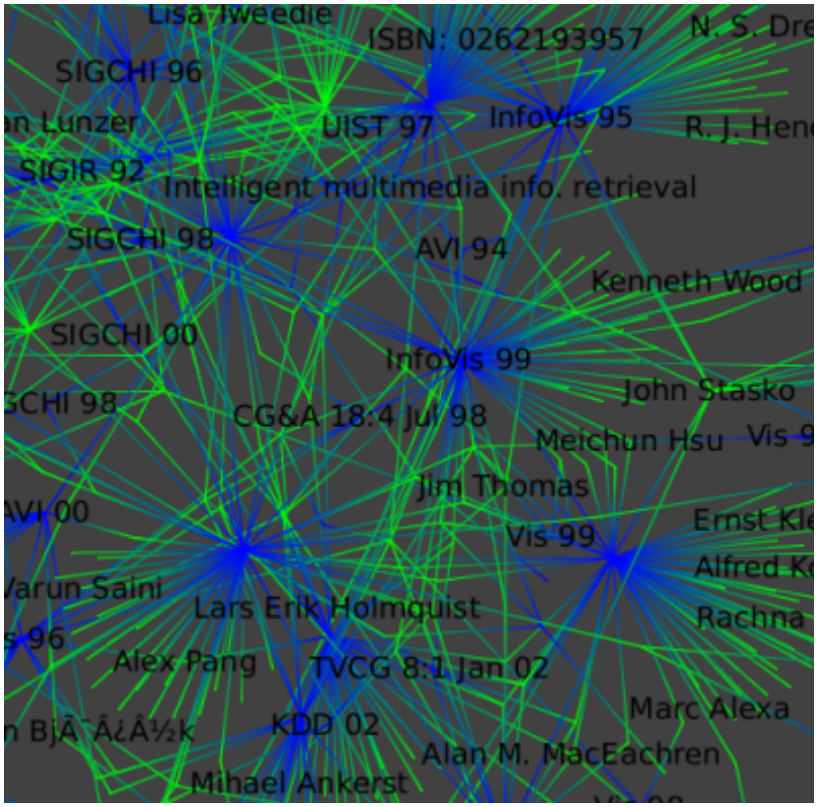
4.3.2.2. Central Authors and Conferences: Overview

To show the large-scale structure of this dataset, we colored Authors in green and conferences in blue with a GEM layout (`Algorithm->Layout->Force Directed->GEM`). We deleted all the papers nodes.



By zooming in :

[6] http://tulip.labri.fr/samples/ConfAuth.tlp.gz

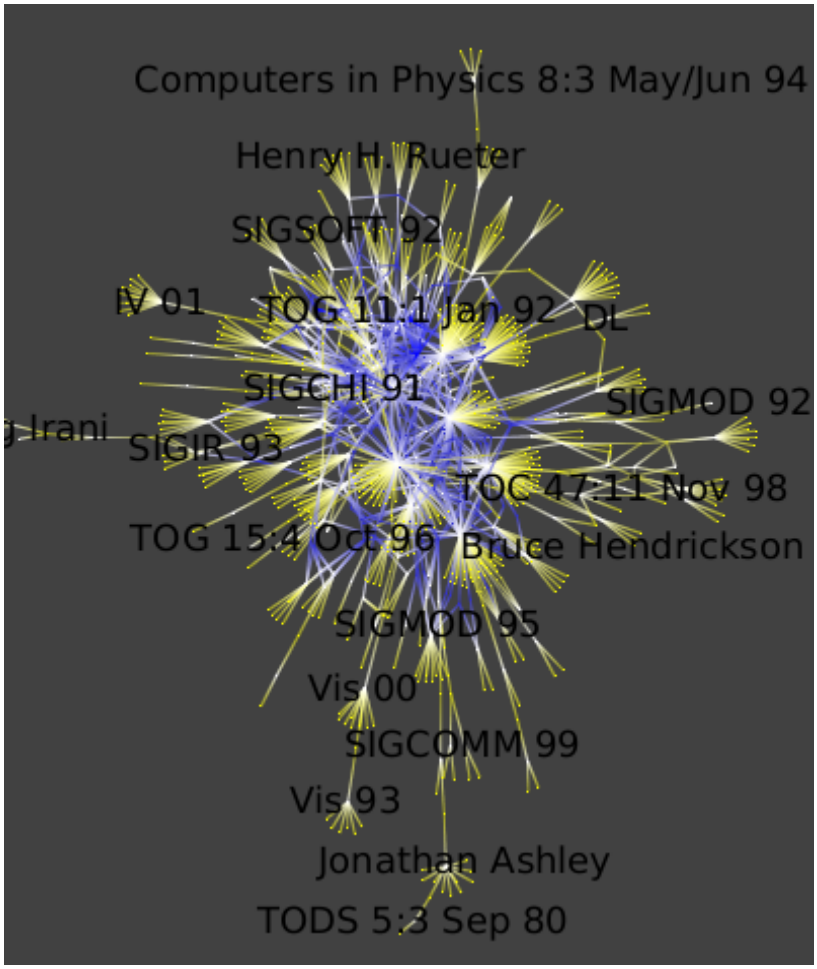


We select only the large connected component (the big set of nodes) : Select a fiew nodes in the center of the component and run the "Reachable Subgraph" selection algorithm with distance set to 50.

Color the authors by the Strahler metric: Run the `Algorithm->Measure->Graph->Strahler` algorithm and then a `Algorithm->Color->Metric Mapping` algorithm.

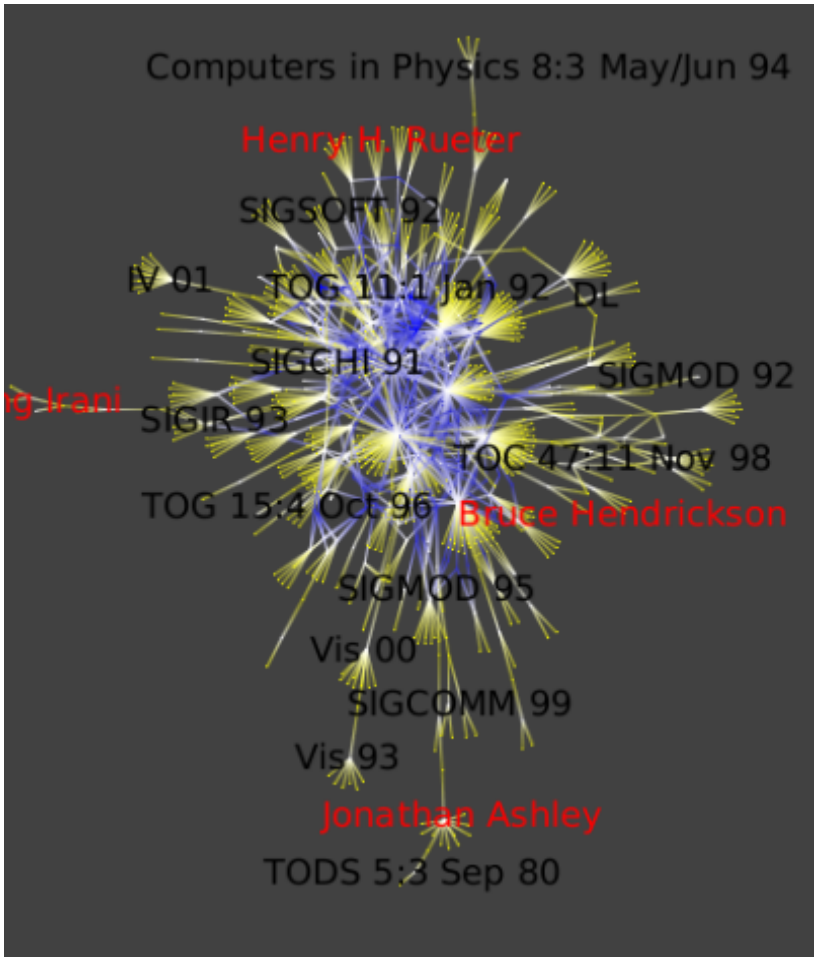
Finally, we color papers in white.

This layout, shows the branching structure of the dataset.



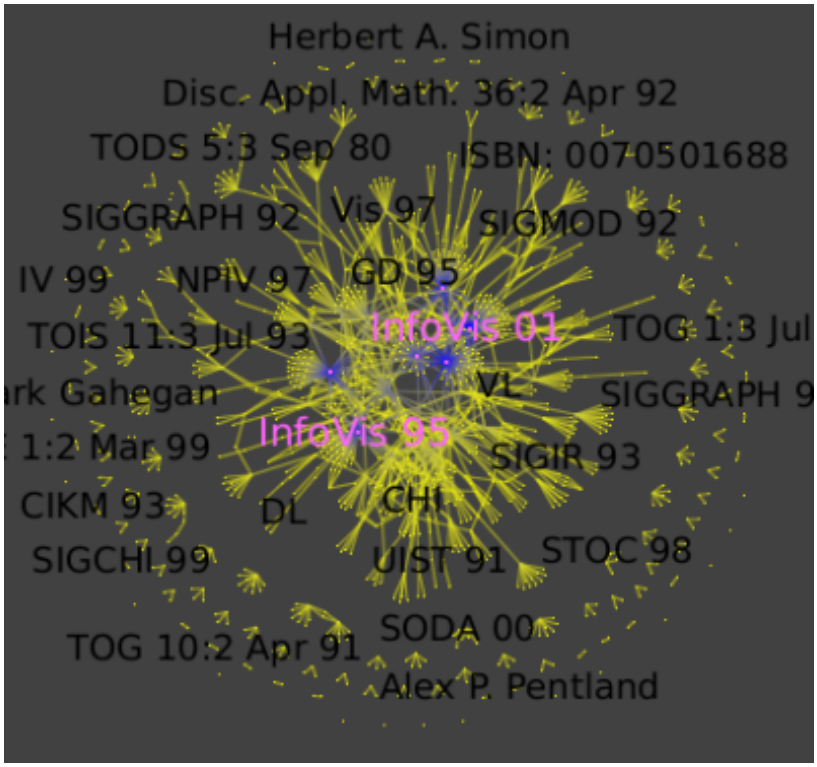
To distinguish authors and conferences :

Select all authors (nodes of type 2) and set their viewLabelColor property to red.



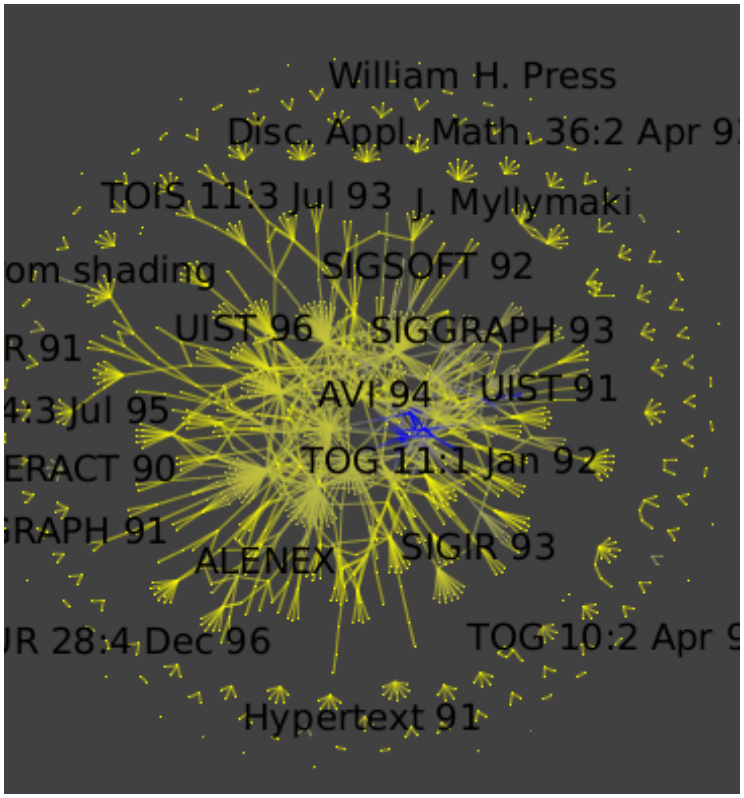
4.3.2.3. Central Authors and Conferences: Top Conferences

It is very simple to see top conferences since they are the ones where the number of authors is high. The Metric Degree will help us to highlight them (`Algorithm->Measure->Graph->Degree`).

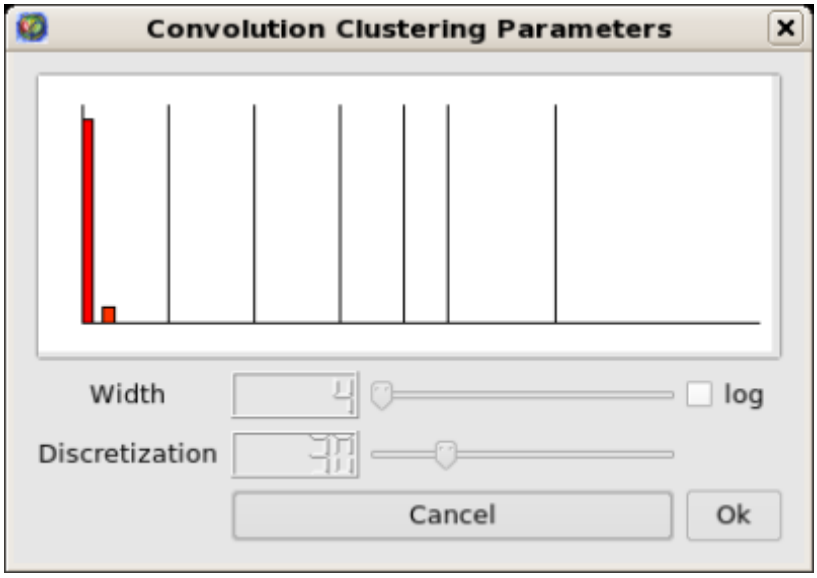


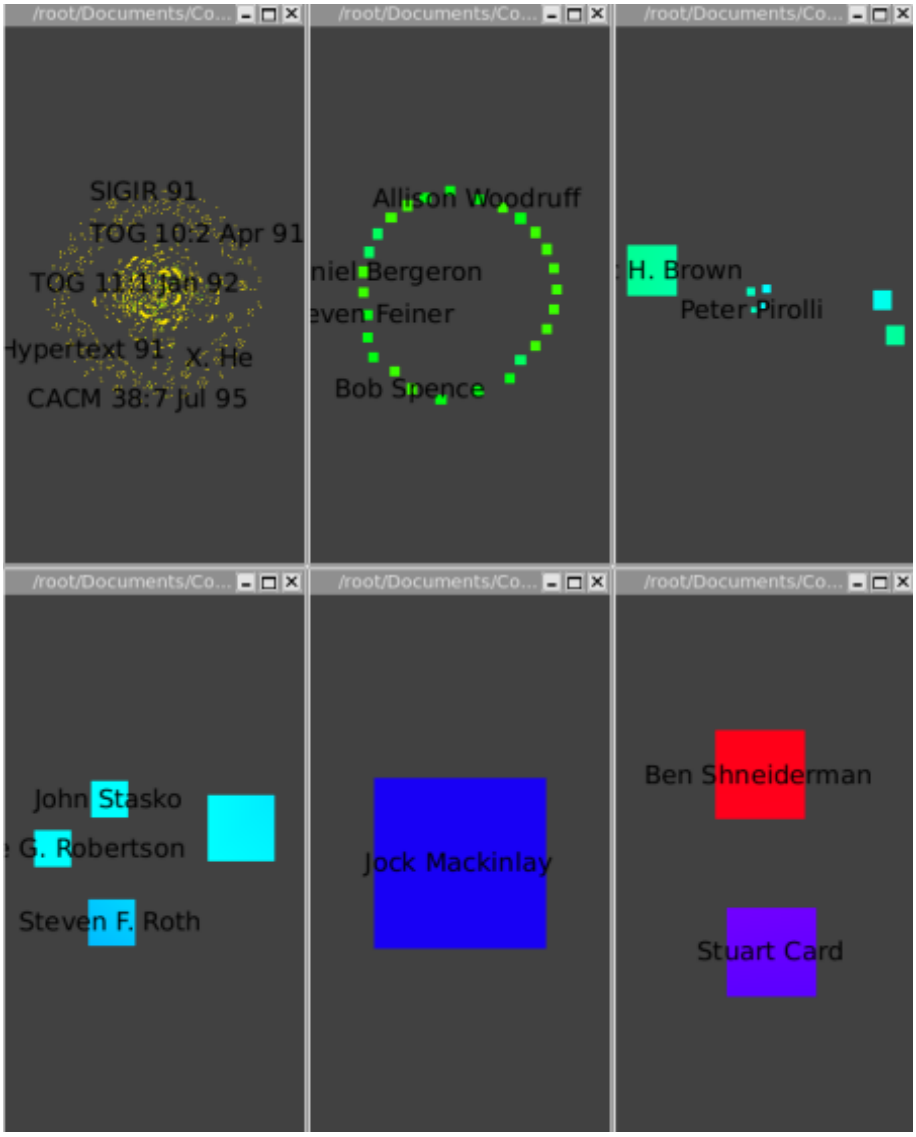
4.3.2.4. Central Authors and Conferences: Top Autors

Run the `Algorithm->Measure->Graph->Strahler` algorithm to see strong ties between conferences and authors :



Then run the `Algorithm->General->Convolution`, the value of the "discretization" parameter should be near 30 to obtain 5 clusters) (Picture 1) to obtain the following clusters (Picture 2):





The Strahler-Convolution clustering yields five clusters, according to increasing centrality. The first cluster is mostly yellow, and contains most of the data. The second cluster contains a next tier of 26 authors that have had

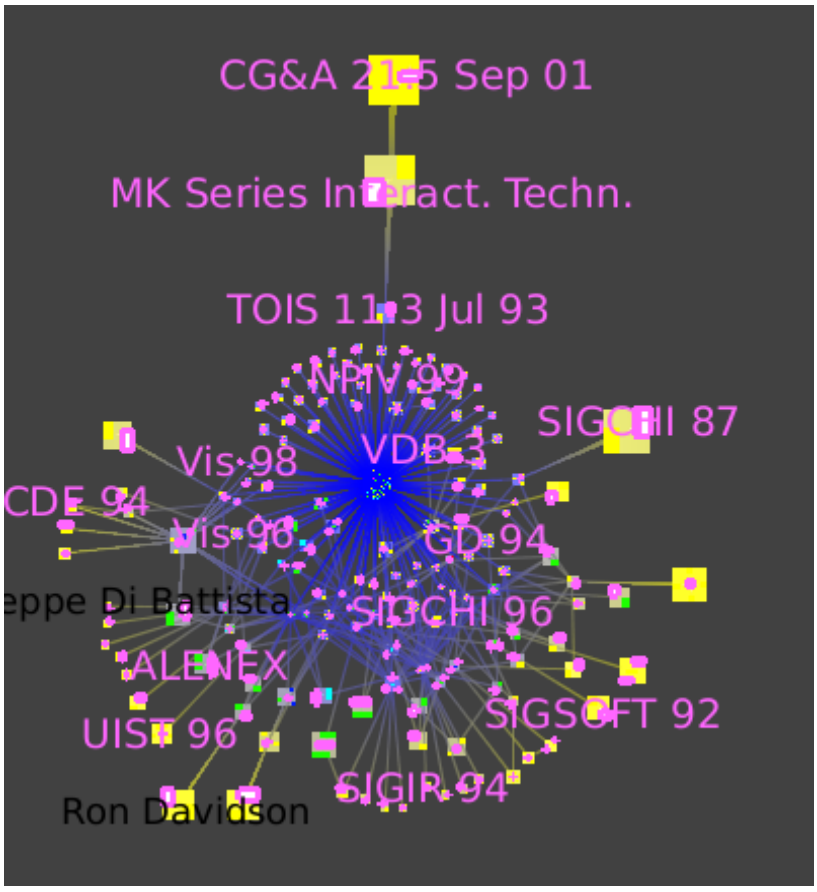
a relatively strong impact. The third cluster contains a group of 7 influential authors (Chi, Bederson, Eick, Rao, Pirolli, Ward, and Brown), and the fourth cluster (Roth, Robertson, Keim, and Stasko) is yet more central. The fifth cluster is the single node of Mackinlay, and the last one is Card and Shneiderman. Our automatic clustering method clearly yields very believeable results in this case.
In the last section, we will use an other graph. Please download it[7] and open it in tulip.

4.3.2.5. Hierarchical Structure of Interauthor Connections

To be able to see the labels within metanode check the "metanode" option in the `Rendering Parameters` dialog (**Ctrl+R**).

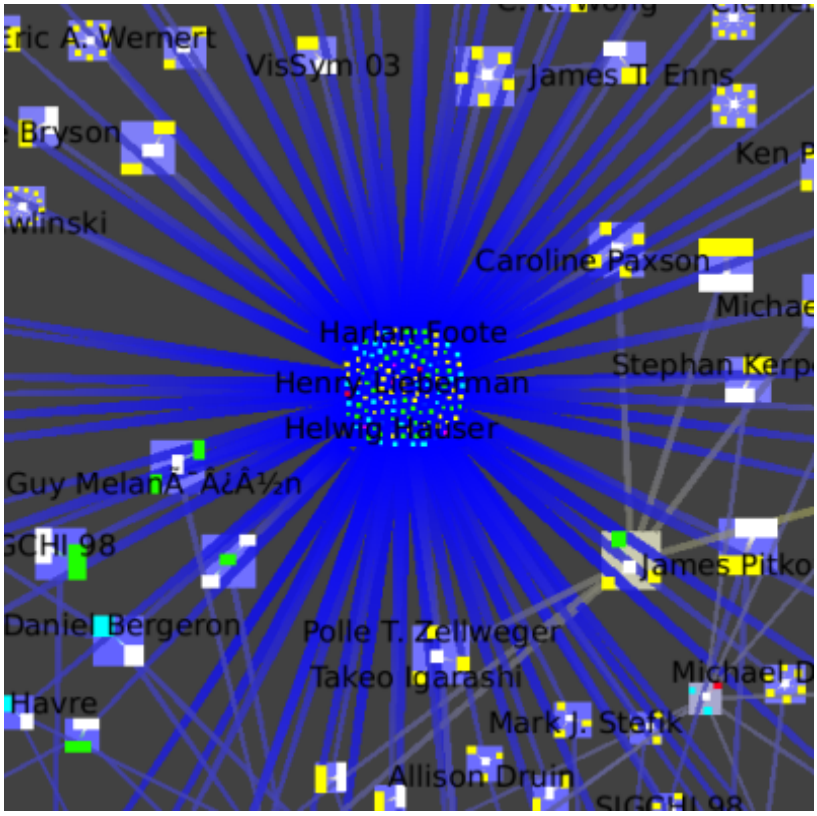
The clusters have been computed using the `Algorithm->General->Strength` clustering algorithm.

The overview image from the previous section, showing the graph of all authors and papers, is extremely cluttered. In the previous task we show one way to extricate more information, by finding the most important items via convolution clustering. Another clustering approach, small-worlds clustering, allows us to instead navigate through a hierarchical subdivision of the entire dataset. The simplified overview allows us to understand the graph's high level structure. The strength metric computes the number of cycles of length 3 and 4 passing through each edge, normalized by the maximum possible value. The first image shows the clustered dataset. Small-world navigation is useful when exploring an unfamiliar graph to quickly find the structure of complex components. The eccentricity metric (`Algorithm->Measure->Graph->Eccentricity`), which measures whether nodes are peripheral (here in yellow) or central (here in blue), guides us to complexity immediately. This metric is O(n^3), but the small-world decomposition simplifies the graph, making the computation tractable.

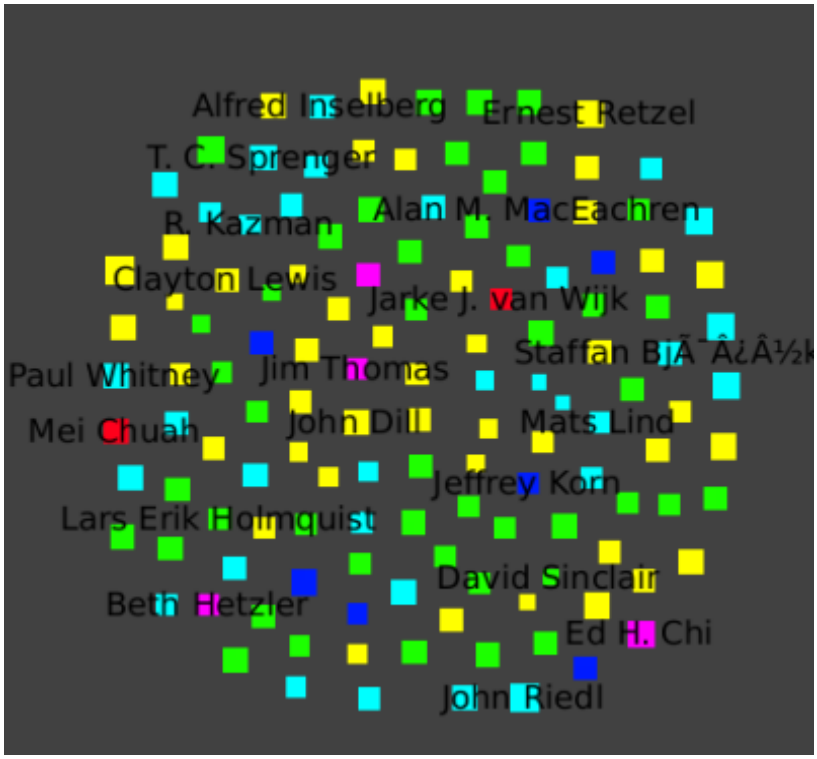


The picture shows zooming in towards the node that has many blue lines leading to it.

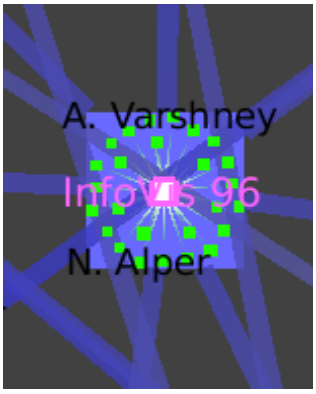
[7] http://tulip.labri.fr/samples/ConfAuthRecSmallWorld.tlp.gz

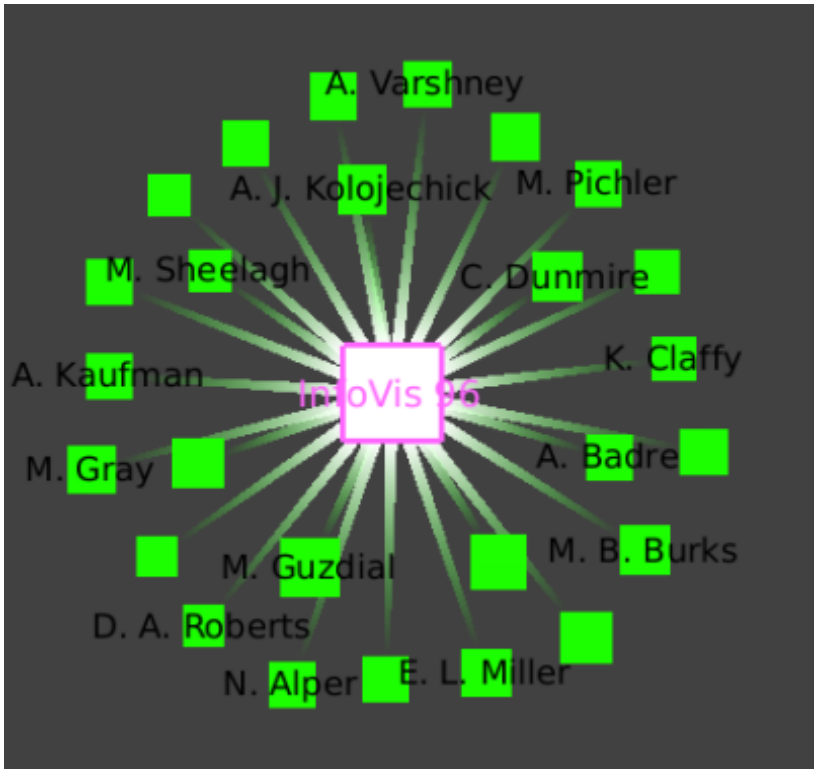


We then jump inside that cluster (Select the metanode, Right Click, Go inside), which is itself a small-world graph.



We once again zoom towards the most central node with many blue edges, where we see a cluster that has the InfoVis 96 conference and all the authors who only published the infovis community in that year.





We see this star shape small-world decomposition only for the InfoVis symposia, because of the nature of this dataset: it is only the InfoVis symposia that have a complete set of authors and papers available.

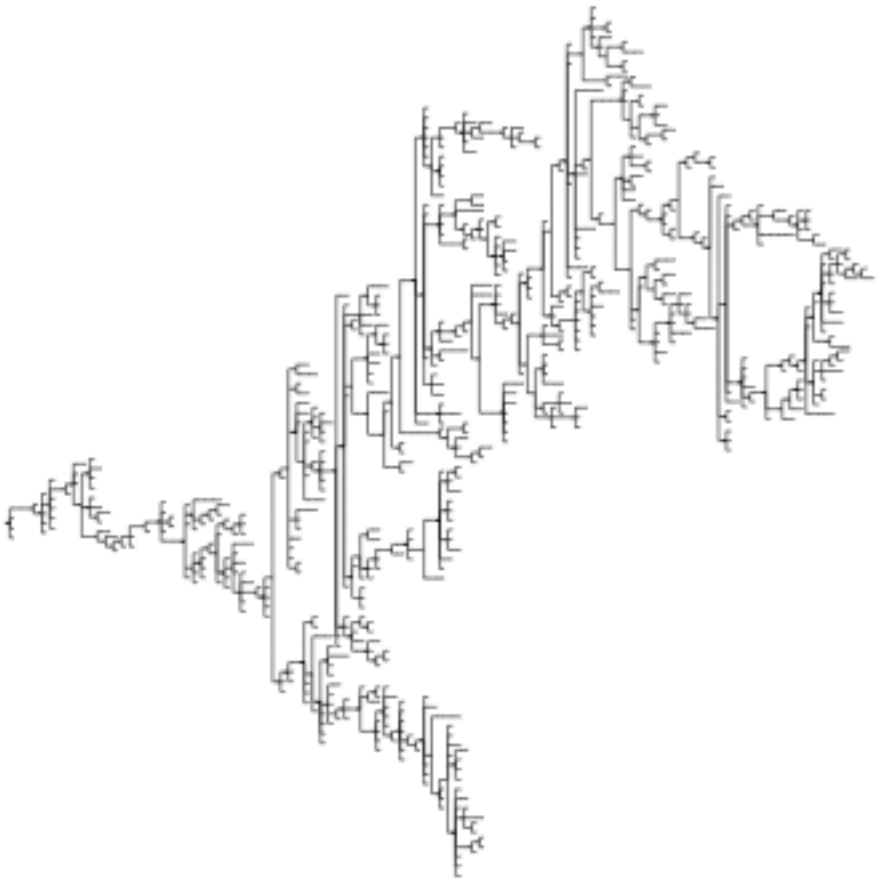
4.4. Statistics Panel (not available in the downloadable binary versions, requires configuration with --enable-stats-gui when compiling Tulip from source code)

4.4.1. Introduction

This section will explain how to use the statistics panel in Tulip. The tutorial is composed of 3 main parts. Firstly, you will see how to generate a scatter plot or an histogram from a graph. In a second part, you will see how to enable augmented displays on the graph. And finally, you will see how to clusterize the graph from the statistics values previously computed.

Every screenshots that will be shown in this tutorial are based on this tree :

Figure 4.1. Statistics base test set : a tree



4.4.2. Scatter plot and Histogram computation

The first thing to understand about the statistics panel is how to generate an histogram or a scatter plot from the graph. The computation of histogram/scatter plot is based on metrics. So, in a first time, you will have to compute metrics. In the example, we have computed three metrics : Arity, DAGLevel and Depth. The new metrics are automatically updated on the *Available Metrics* list on the Stats panel :

Figure 4.2. The metrics available in the statistics panel

Now that you have some metrics available. You can add them to the *Used Metrics* list simply using the *Add* and *Remove* buttons. The number of dimensions of the result will only depend of the numbers of metrics you add to the list. With only one metric added, you will have an frequency histogram displayed. With two (resp three) metrics you will have a 2D (resp. 3D) scatter plot. Each metric representing a different dimension.

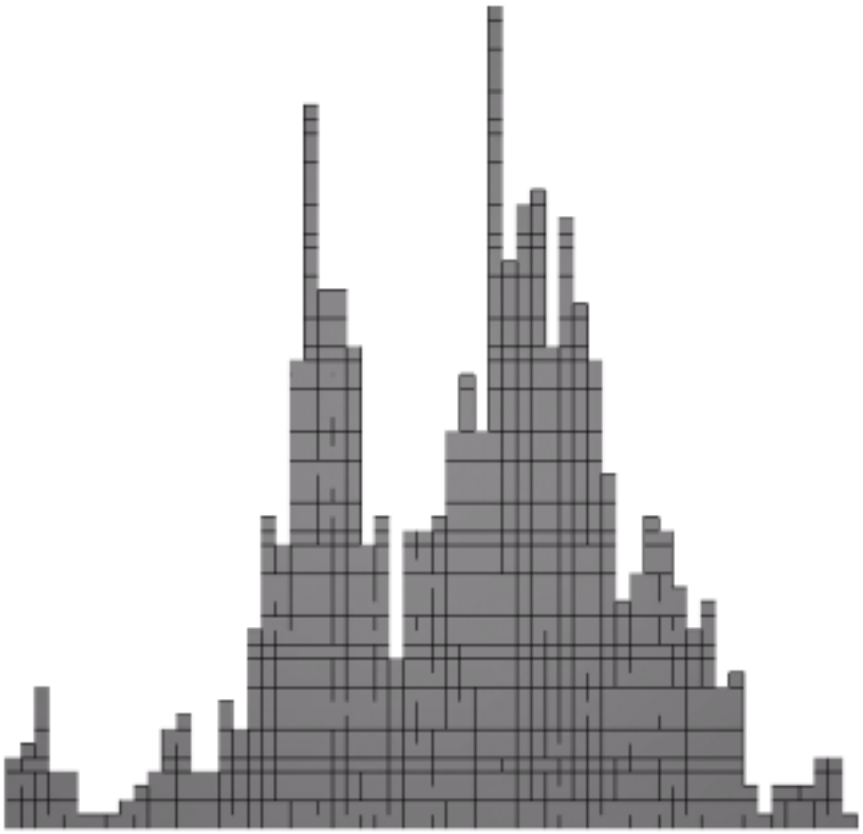
In the example, we have only added the *DAGLevel* metric to the *Used Metrics* list :

Figure 4.3. A single metric for an histogram

As you can see, adding a metric implies some changes in the interface. The bottom button becomes enabled, so as the edit box corresponding to *Discretization Step 1*. You can specify a discretization step, even if it is not really useful for our example.

Now the last step before having a beautiful frequency histogram displayed : asking the panel to compute it. Just click on the *Compute Histogram* button. That's it !!! You have your first histogram : congratulations !!!

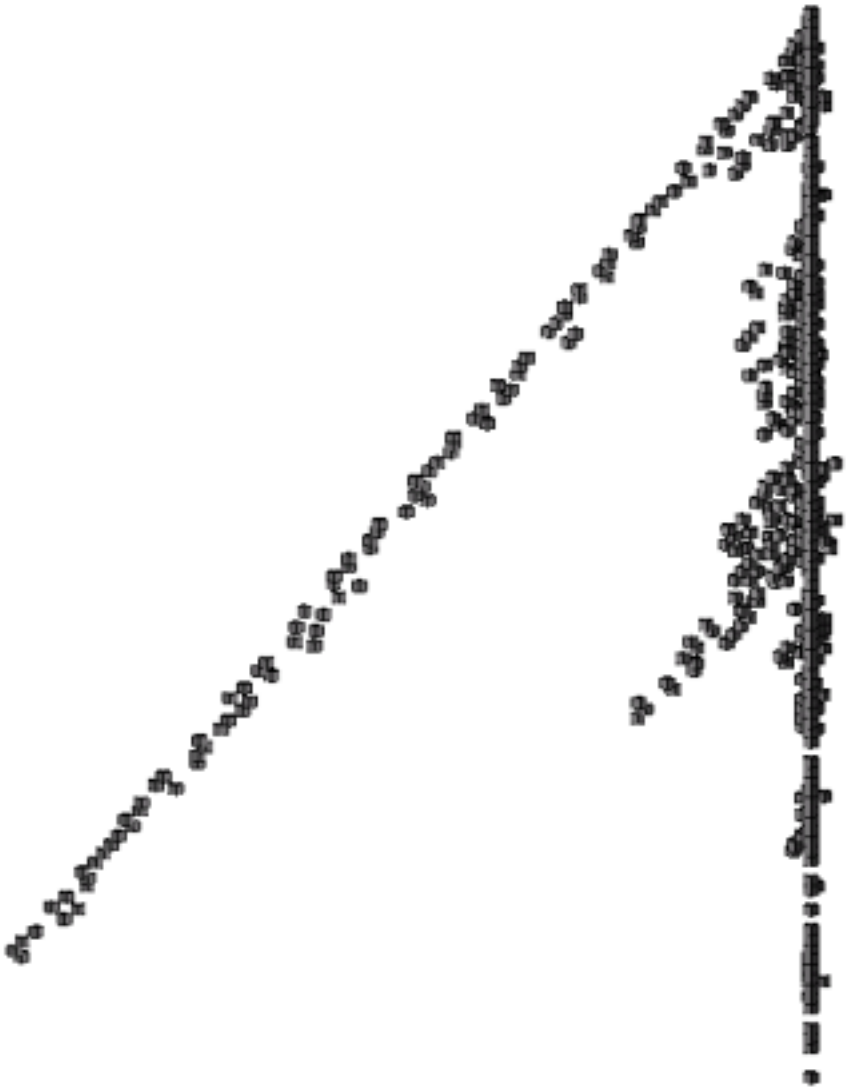
Figure 4.4. Your first histogram



Now that we have an histogram. We are not going to stop here. Let's generate a scatter plot in three dimensions. Just add two other metrics to the *Used Metrics* list. You will notice that the text of the *Compute Histogram* button now becomes *Compute Scatter Plot*. Just click it and you will have a scatter plot.

Here is the result with our base tree and the three metrics mentionned in the introduction :

Figure 4.5. Scatter plot generated from the three metrics

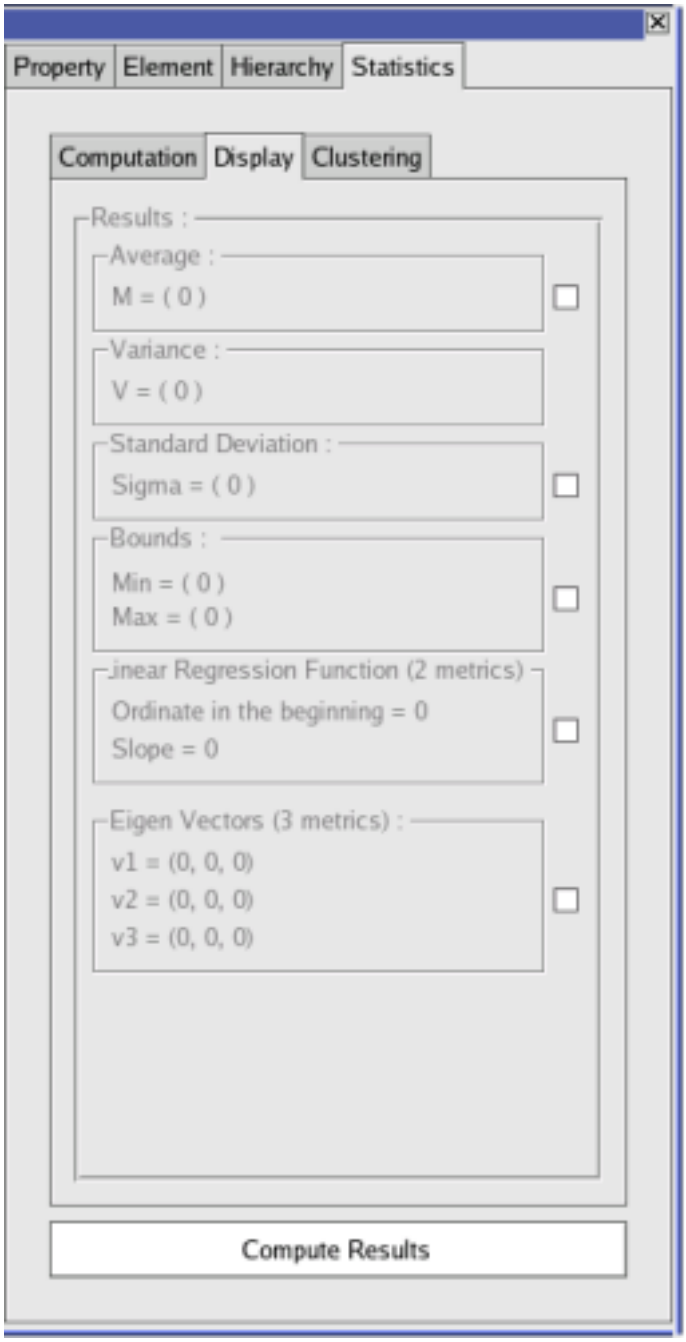


As a conclusion to this first part, you have learnt how to generate a simple frequency histogram from a graph and a metric. You have also learnt how to generate a whole scatter plot from 2 to 3 metrics. In the next part, you will learn how to display the basic statical values on the graph.

4.4.3. Statistics values and Augmented displays

Now, we will see how to compute the main statistics results, and how to display them on the generated Histogram/Scatter Plot. Switch to the *Display* tab of the statistics panel. Yet, everything is grayed. To compute the values of the tab, you must click on the bottom button *Compute Results*. Note that this button is reachable on every tab on the panel but you will be able to click it only if the *Used Metrics* list of the *Computation* tab is not empty.

Figure 4.6. Click on the button Compute Result to enable the tab



Once the results computed, most of the elements of the panel should be enabled. Note that the *Regression Function* group is enabled only if you hase two metrics in the *Used Metrics* list, and *Eigenvectors* is enabled only if you have three metrics in the *Used Metrics* list.

The checkboxes next to each groupboxes (except the *Variance* one) are used to display on the Histogram/Scatter plot, the result of the group. For example : checking the checkbox next to *Average* will display the average point on the graph (an Axis Point in red (c.f. GlAugmentedDisplay in the developer handbook)).

Figure 4.7. Checking Average on the display tab

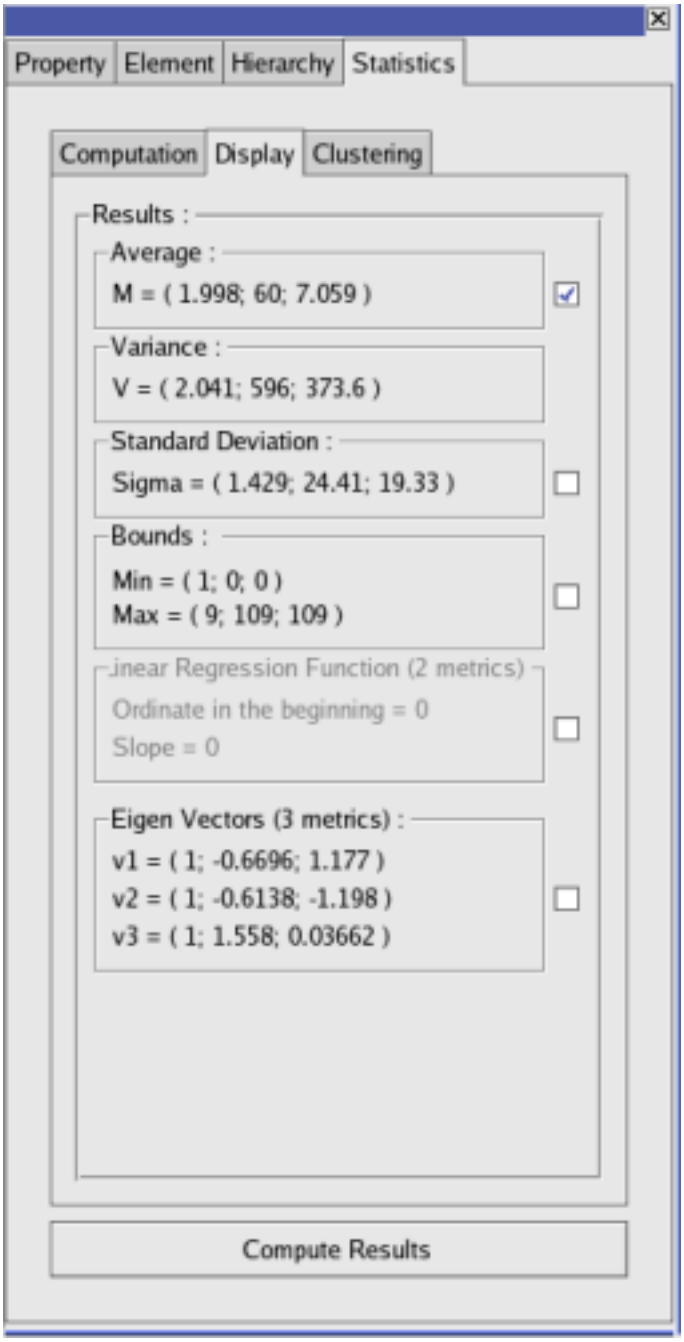
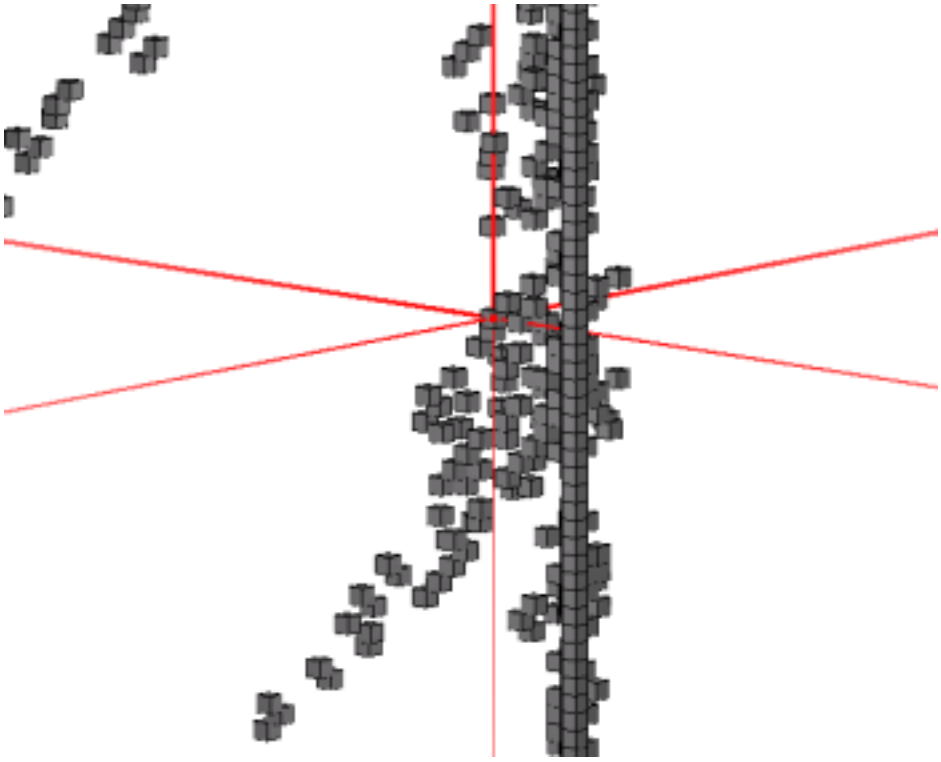


Figure 4.8. The average of the scatter plot



Every augmented display works the same way. You will just have to click on the checkbox next to the group to enable the display of the result. Note that you can't display the Variance since this result can't be represented in an interesting way on the graph. use instead the standard deviation.

Now that you know how to display the statistics results, you will see how to clusterize the scatter plot / histogram from these values.

4.4.4. Clustering with the statistics panel

The last part of this tutorial will teach you how to clusterize from the statistics results previously computed. Firstly, switch to the *Clustering* tab. The Combobox *Clustering Value* lists the available start for a clustering plane depending on what has been computed before. Select *Average (Z)*(you must have selected 3 metrics), the plane coordinates will be modified according to the values of the average's Z coordinate. Check the *Display Clustering Plane* checkbox. The plane appears in transparent red, showing you the future two clusters.

Figure 4.9. Selection of the clustering value

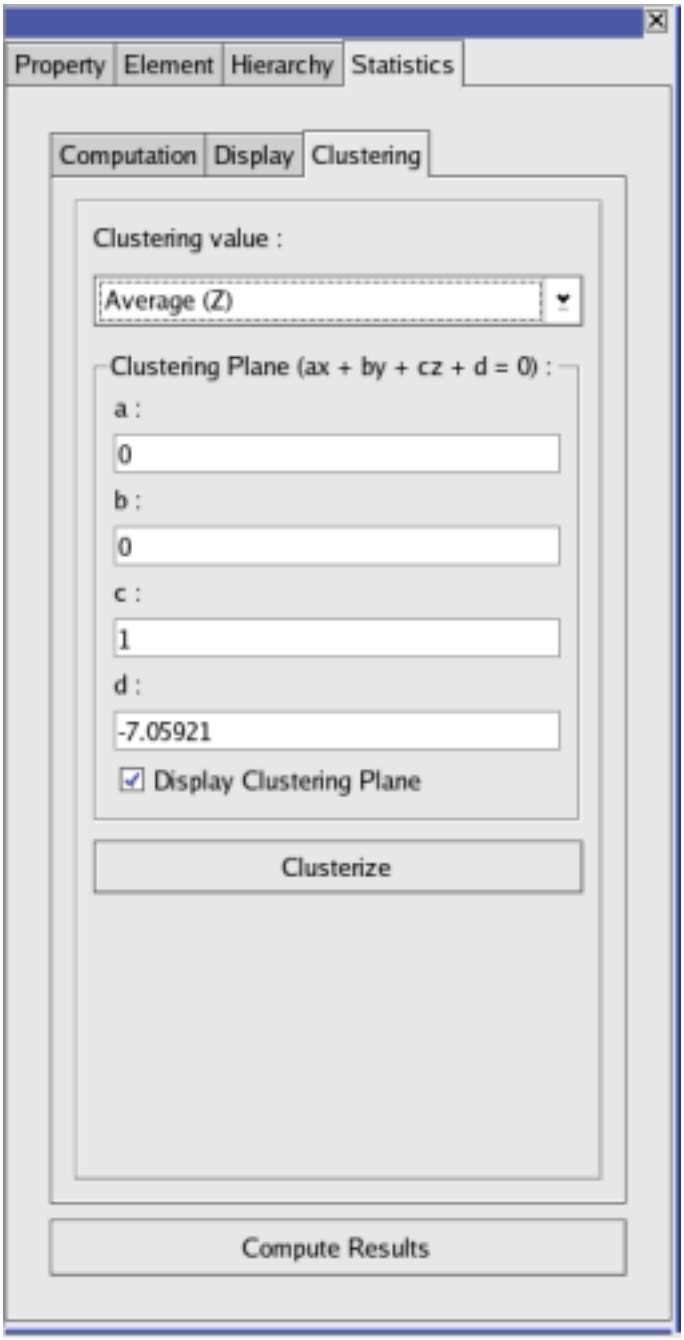
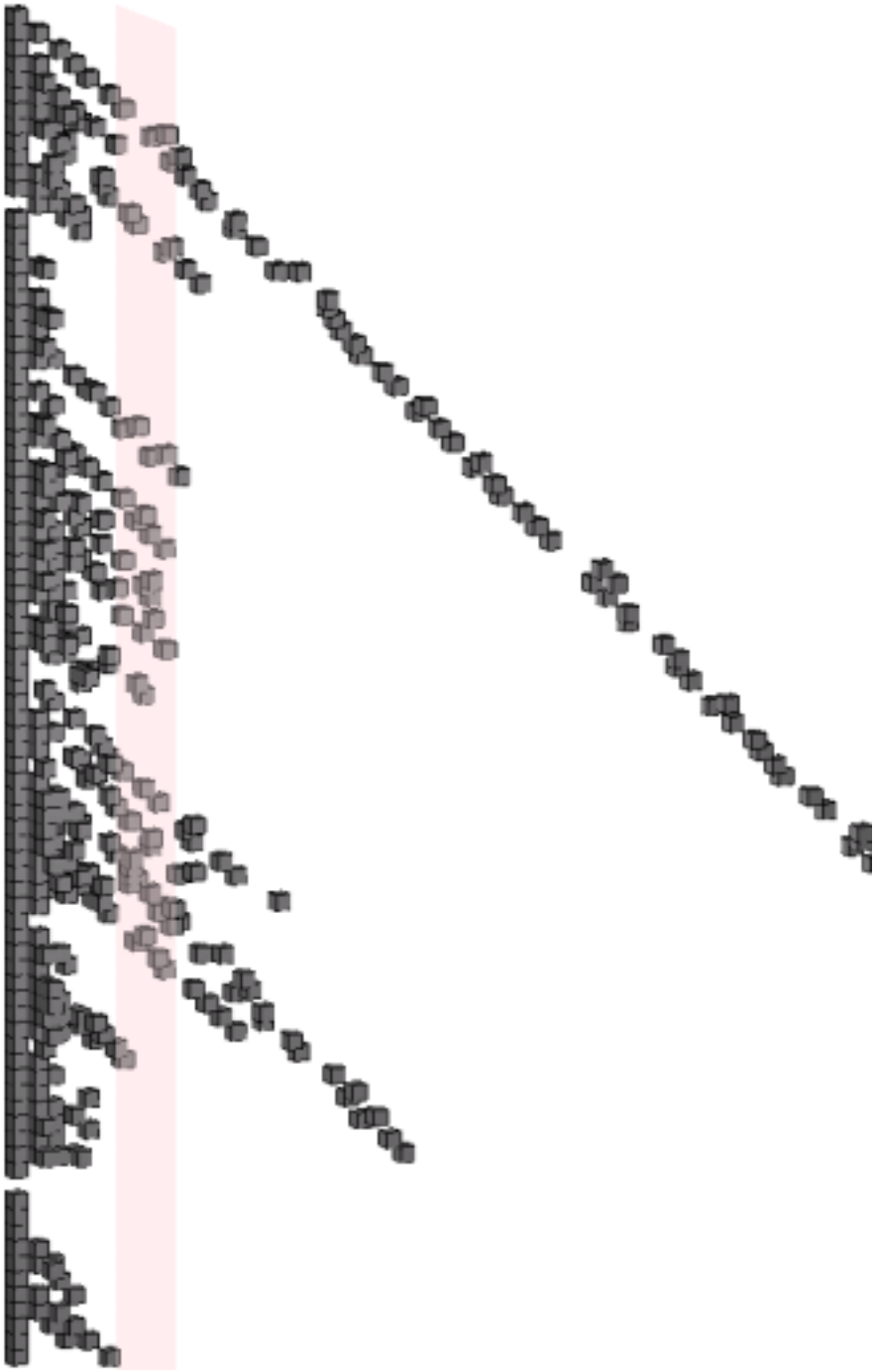
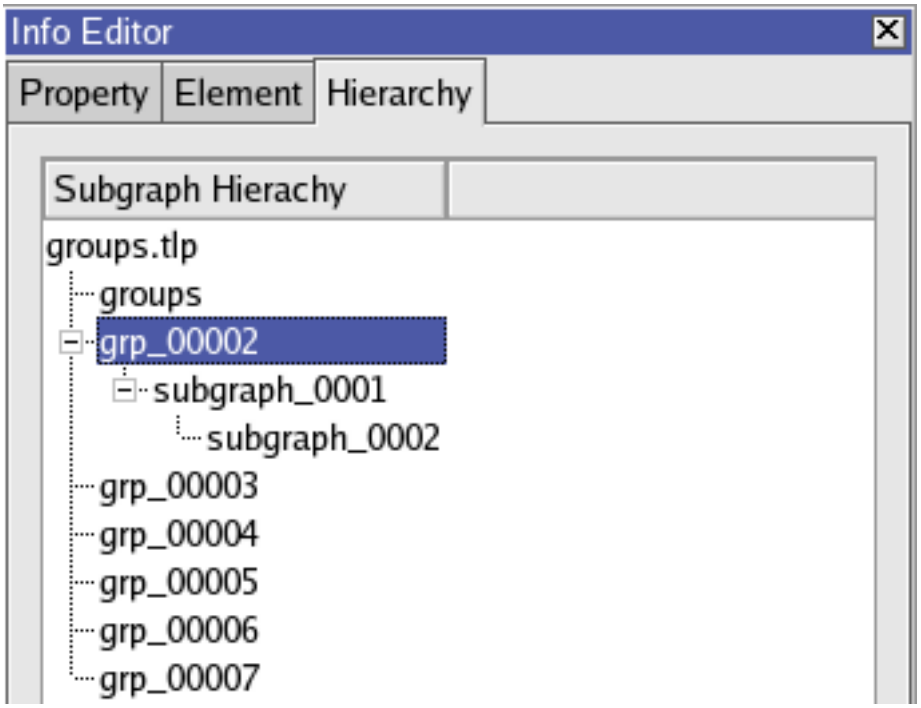


Figure 4.10. The clustering plane



In order to have the good clustering, you can modify the plane equation (not really smooth : will be enhanced in the next versions of Tulip) to move the plane. Finally, to clusterize, just click on the *Clusterize* button. That's it ! The graph is now clusterized. In order to ensure, just check the *Cluster Tree*.

Figure 4.11. The new clusters after statistic clustering



4.4.5. Conclusion

As a conclusion, you have learnt how to use the statistics panel of Tulip. As you can see, obtaining results is easy and fast. If you have any question about that panel, you can contact it's creator at <maxime.delorme@gmail.com>